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<b>(21) International Application Number:</b> PCT/GB96/01332 <b>(22) International Filing Date:</b> 3 June 1996 (03.06.96)  <b>(30) Priority Data:</b> 9511196.9      2 June 1995 (02.06.95)      GB  <b>(71) Applicant (for all designated States except US):</b> JOHN INNES CENTRE INNOVATIONS LIMITED [GB/GB]; Norwich Research Park, Colney Lane, Norwich NR4 7UH (GB).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> DEAN, Caroline [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). MACKNIGHT, Richard, Colin [NZ/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). BANCROFT, Ian [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). LISTER, Clare, Katharine [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB).  <b>(74) Agents:</b> WALTON, Seán, M. et al.; Mewburn Ellis, York House, 23 Kingsway, London WC2B 6HP (GB).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> GENETIC CONTROL OF FLOWERING  <b>(57) Abstract</b>  <i>FCA genes of Arabidopsis thaliana and Brassica napus are provided, enabling flowering characteristics, particularly timing of flowering, to be influenced in transgenic plants. Timing of flowering may be delayed or hastened using sense and antisense expression, also various mutants and alleles, including alternatively spliced forms.</i>		

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## GENETIC CONTROL OF FLOWERING

This invention relates to the genetic control of flowering in plants and the cloning and expression of genes involved therein. More particularly, the invention  
5 relates to the cloning and expression of the FCA gene of *Arabidopsis thaliana*, and homologues from other species, and manipulation and use of these genes in plants.

Efficient flowering in plants is important, particularly when the intended product is the flower or  
10 the seed produced therefrom. One aspect of this is the timing of flowering: advancing or retarding the onset of flowering can be useful to farmers and seed producers. An understanding of the genetic mechanisms which influence flowering provides a means for altering the flowering  
15 characteristics of the target plant. Species for which flowering is important to crop production are numerous, essentially all crops which are grown from seed, with important examples being the cereals, rice and maize, probably the most agronomically important in warmer  
20 climatic zones, and wheat, barley, oats and rye in more temperate climates. Important seed products are oil seed rape, sugar beet, maize, sunflower, soybean and sorghum. Many crops which are harvested for their roots are, of course, grown annually from seed and the production of  
25 seed of any kind is very dependent upon the ability of the plant to flower, to be pollinated and to set seed. In horticulture, control of the timing of flowering is important. Horticultural plants whose flowering may be

controlled include lettuce, endive and vegetable brassicas including cabbage, broccoli and cauliflower, and carnations and geraniums.

*Arabidopsis thaliana* is a facultative long-day plant, flowering early under long days and late under short days. Because it has a small, well-characterized genome, is relatively easily transformed and regenerated and has a rapid growing cycle, *Arabidopsis* is an ideal model plant in which to study flowering and its control.

One of the genes required for rapid floral induction is the *FCA* gene (Koornneef et al 1991). Plants carrying mutations of this gene flower much later than wild-type under long photoperiods and short photoperiods. There is a considerable range in flowering time within different mutant *fca* alleles. The most extreme (*fca-1*) flowers under long photoperiods with up to 40 leaves whereas *fca-3*, *fca-4* flower with ~20 rosette leaves compared to 9 for wild-type *Landsberg erecta*). The late flowering of all the *fca* mutants can be overcome to early flowering in both long and short photoperiods if imbibed seeds, or plants of different developmental ages, are given 3-8 weeks at 4°C - a vernalization treatment (Chandler and Dean 1994).

We have cloned and sequenced the *FCA* gene of *Arabidopsis thaliana*, a homologue from *Brassica* and mutant sequences.

According to a first aspect of the present invention there is provided a nucleic acid molecule comprising a

nucleotide sequence encoding a polypeptide with *FCA* function. Those skilled in the art will appreciate that "FCA function" refers to the ability to influence the timing of flowering phenotypically like the *FCA*-gene of *Arabidopsis thaliana*, especially the ability to complement an *fca* mutation in *Arabidopsis thaliana*.

Nucleic acid according to the invention may encode a polypeptide comprising the amino acid sequence shown in Figure 2, or an allele, variant, derivative or mutant thereof. Particular variants include those wherein the amino acid residues up-stream of the third methionine and/or up-stream of the second methionine in the amino acid sequence of Figure 2 are not included. Variants, mutants and derivatives of nucleic acid encoding such shorter polypeptide are of course provided by various embodiments of the present invention.

Nucleic acid according to the present invention may have the sequence of an *FCA* gene of *Arabidopsis thaliana*, or be a mutant, variant (or derivative) or allele of the sequence provided. Preferred mutants, variants and alleles are those which encode a protein which retains a functional characteristic of the protein encoded by the wild-type gene, especially the ability to promote flowering as discussed herein. Promotion of flowering may advance, hasten or quicken flowering. Other preferred mutants, variants and alleles encode a protein which delays flowering compared to wild-type or a gene with the sequence provided. Changes to a sequence, to

produce a mutant or variant, may be by one or more of insertion, deletion or substitution of one or more nucleotides in the nucleic acid, leading to the insertion, deletion or substitution of one or more amino acids. Of course, changes to the nucleic acid which make no difference to the encoded amino acid sequence are included. Particular variants, mutants, alleles and variants are discussed further below.

A preferred nucleic acid sequence covering the region encoding the FCA gene is shown in Figure 1 and the predicted amino acid sequence encoding the FCA ORF is shown in Figure 2. Nucleic acid may be subject to alteration by way of substitution of nucleotides and/or a combination of addition, insertion and/or substitution of one or more nucleotides with or without altering the encoded amino acids sequence (by virtue of the degeneracy of the genetic code).

Nucleic acid according to the present invention may comprise an intron, such as an intron shown in Figure 1, for instance intron 3 (as in various embodiments e.g. as illustrated herein), whether or not the encoded amino acid sequence is altered. For example, the variant FCA  $\alpha_B$ , whose nucleic acid sequence is shown in Figure 3, comprises intron 3 of the sequence of Figure 1, such that translation of the sequence results in a different amino acid sequence from that of Figure 2 (intron 3 of Figure 1 contains a stop codon at 3026-3028 that is potentially used in transcripts).

The present invention also provides a vector which comprises nucleic acid with any one of the provided sequences, preferably a vector from which polypeptide encoded by the nucleic acid sequence can be expressed.

5 The vector is preferably suitable for transformation into a plant cell. The invention further encompasses a host cell transformed with such a vector, especially a plant cell. Thus, a host cell, such as a plant cell, comprising nucleic acid according to the present invention is  
10 provided. Within the cell, the nucleic acid may be incorporated within the chromosome. There may be more than one heterologous nucleotide sequence per haploid genome. This, for example, enables increased expression of the gene product compared with endogenous levels, as  
15 discussed below.

A vector comprising nucleic acid according to the present invention need not include a promoter, particularly if the vector is to be used to introduce the nucleic acid into cells for recombination into the  
20 genome.

Nucleic acid molecules and vectors according to the present invention may be provided isolated and/or purified from their natural environment, in substantially pure or homogeneous form, or free or substantially free  
25 of nucleic acid or genes of the species of interest or origin other than the sequence encoding a polypeptide able to influence flowering, eg in *Arabidopsis thaliana* nucleic acid other than the FCA sequence. Nucleic acid

according to the present invention may comprise cDNA, RNA, genomic DNA and may be wholly or partially synthetic. The term "isolate" may encompass all these possibilities.

5           The present invention also encompasses the expression product of any of the nucleic acid sequences disclosed and methods of making the expression product by expression from encoding nucleic acid therefore under suitable conditions in suitable host cells, e.g. *E. coli*  
10 (see Example 7). Those skilled in the art are well able to construct vectors and design protocols for expression and recovery of products of recombinant gene expression. Suitable vectors can be chosen or constructed, containing one or more appropriate regulatory sequences, including  
15 promoter sequences, terminator fragments, polyadenylation sequences, enhancer sequences, marker genes and other sequences as appropriate. For further details see, for example, *Molecular Cloning: a Laboratory Manual*: 2nd edition, Sambrook et al, 1989, Cold Spring Harbor  
20 Laboratory Press. Transformation procedures depend on the host used, but are well known. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene  
25 expression, and analysis of proteins, are described in detail in *Short Protocols in Molecular Biology*, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992.



The disclosures of Sambrook et al. and Ausubel et al. are incorporated herein by reference.

Purified FCA protein, or a fragment, mutant or variant thereof, e.g. produced recombinantly by

5 expression from encoding nucleic acid therefor, may be used to raise antibodies employing techniques which are standard in the art, as exemplified in Example 7. Antibodies and polypeptides comprising antigen-binding fragments of antibodies may be used in identifying  
10 homologues from other species as discussed further below.

Methods of producing antibodies include immunising a mammal (eg human, mouse, rat, rabbit, horse, goat, sheep or monkey) with the protein or a fragment thereof.

Antibodies may be obtained from immunised animals using  
15 any of a variety of techniques known in the art, and might be screened, preferably using binding of antibody to antigen of interest. For instance, Western blotting techniques or immunoprecipitation may be used. (Armitage et al, 1992, Nature 357: 80-82). Antibodies may be  
20 polyclonal or monoclonal.

As an alternative or supplement to immunising a mammal, antibodies with appropriate binding specificity may be obtained from a recombinantly produced library of expressed immunoglobulin variable domains, eg using  
25 lambda bacteriophage or filamentous bacteriophage which display functional immunoglobulin binding domains on their surfaces; for instance see WO92/01047.

Antibodies raised to a polypeptide or peptide can be used in the identification and/or isolation of homologous polypeptides, and then the encoding genes. Thus, the present invention provides a method of identifying or  
5 isolating a polypeptide with FCA function (in accordance with embodiments disclosed herein), comprising screening candidate polypeptides with a polypeptide comprising the antigen-binding domain of an antibody (for example whole antibody or a fragment thereof) which is able to bind an  
10 FCA polypeptide or fragment, variant or variant thereof or preferably has binding specificity for such a polypeptide, such as having the amino acid sequence shown in Figure 2 or Figure 8b. Specific binding members such as antibodies and polypeptides comprising antigen binding  
15 domains of antibodies that bind and are preferably specific for a FCA polypeptide or mutant, variant or derivative thereof represent further aspects of the present invention, as do their use and methods which employ them.

20 Candidate polypeptides for screening may for instance be the products of an expression library created using nucleic acid derived from an plant of interest, or may be the product of a purification process from a natural source.

25 A polypeptide found to bind the antibody may be isolated and then may be subject to amino acid sequencing. Any suitable technique may be used to sequence the polypeptide either wholly or partially (for

instance a fragment of the polypeptide may be sequenced). Amino acid sequence information may be used in obtaining nucleic acid encoding the polypeptide, for instance by designing one or more oligonucleotides (e.g. a degenerate pool of oligonucleotides) for use as probes or primers in hybridisation to candidate nucleic acid, or by searching computer sequence databases, as discussed further below.

The present invention further encompasses a plant comprising a plant cell comprising nucleic acid according to the present invention e.g. as a result of introduction of the nucleic acid into the cell or an ancestor thereof, and selfed or hybrid progeny and any descendent of such a plant, also any part or propagule of such a plant, progeny or descendant, including seed.

The FCA gene encodes a large protein (796 amino acids shown in Figure 2) with homology to a class of proteins identified as RNA-binding proteins (Burd and Dreyfuss 1994). These proteins contain 80 amino acid, RNA recognition motifs (RRMs) and have a modular structure- they can contain several RNA binding domains and auxiliary domains rich in amino acids such as glycine, glutamine and proline. The RRM proteins can be divided into subfamilies based on homology within and around the RRM domains. The FCA protein is most homologous to a subfamily of RNA-binding proteins (cluster 1028.16; identified using the BEAUTY database search, Worley et al., 1995) exemplified by the *Drosophila elav* gene (Robinow et al., 1988). Other members of this family

include the *Drosophila* sexlethal protein; the human nervous system proteins HuD, HuC, Hel-N1, and Hel-N2; and the *Xenopus* proteins elrA, elrB, elrC, elrD and etr-1. FCA has two RNA-binding domains while most of the members of elav gene family have three RNA-binding domains. The first two RNA-binding domains of elav family (and the spacing between the domains) is similar to the RNA-binding domains in the FCA protein. In common with the FCA protein the elav has a region with high glutamine content. There is also a 20 amino acid region near the C terminus of the FCA protein which shows strong homology to ORFs from two genes of unknown function from yeast and *C. elegans*.

The FCA transcript is alternatively spliced. Five forms of the transcript are generated in cells. One, herein called FCA transcript  $\beta$  is ~ 2kb and represents premature termination and polyadenylation within intron 3. FCA  $\alpha_A$  and  $\alpha_B$  has 19 of 20 introns spliced out but intron 3 (2kb) remaining. FCA  $\alpha_A$  is the same as  $\alpha_B$  except at intron 11 where different 5' and 3' exon/intron junctions are used. FCA  $\alpha_A$  uses the 5' exon/intron junction at 7055 bp (genomic sequence Fig.1) and 3' exon/intron junction at 7377 bp. FCA  $\alpha_B$  uses the 5' exon/intron junction at 7130 bp (genomic sequence Fig.1) and 3' exon/intron junction at 7295 bp. FCA transcripts  $\gamma_A$  and  $\gamma_B$  both have intron 3 removed and  $\gamma_A$  and  $\gamma_B$  use the same junctions around intron 11 as  $\alpha_A$  and  $\alpha_B$ .

respectively. Only  $\gamma_B$  encodes both RNA-binding domains and the conserved C-terminal domain (Figure 10).

RNA-binding proteins have been shown to be involved in several facets of post-transcriptional regulation. The RNP motif forms a  $\beta$  sheet RNA binding surface engaging the RNA as an open platform for interaction with either other RNA molecules or other proteins. One of the most well characterized genes encoding an RNP motif-containing protein is the *Drosophila* *SEX-LETHAL* gene (Bell et al 1988). The *SEX-LETHAL* protein is involved in altering the splicing of its own and other transcripts within the pathway that determines sex in *Drosophila*. Only the alternatively spliced product gives an active protein. Thus this gene product is responsible for determining and maintaining the female state. Other RNA-binding proteins have been shown to function by localizing specific transcripts in the nucleus or preventing translation of specific transcripts. Six independently isolated *fca* mutants have been described, and we have identified the sequence changes causing a reduction in *FCA* activity in three cases. The *fca-1* mutation converted a C nucleotide at position 6861 (Figure 1) into a T. Thus a glutamine codon (CAA) is changed into a stop codon (TAA). The *fca-3* mutation converted a G nucleotide at position 5271 into an A. The effect of this mutation is to alter the 3' splice junction of intron 7 such that a new 3' splice junction is used 28 nucleotides into exon 8. The *fca-4* mutation is the result of a rearrangement (an inversion

taking the 3' end of the gene 250kb away) with the break-point at position 4570 (within intron 4).

A further aspect of the present invention provides a method of identifying and cloning *FCA* homologues from  
5 plant species other than *Arabidopsis thaliana* which method employs a nucleotide sequence derived from that shown in Figure 1. Nucleic acid libraries may be screened using techniques well known to those skilled in the art and homologous sequences thereby identified then tested.  
10 The provision of sequence information for the *FCA* gene of *Arabidopsis thaliana* enables the obtention of homologous sequences from *Arabidopsis* and other plant species. In Southern hybridization experiments a probe containing the *FCA* gene of *Arabidopsis thaliana* hybridises to DNA  
15 extracted from *Brassica rapa*, *Brassica napus* and *Brassica oleraceae*. In contrast to most *Arabidopsis* genes, which are normally present on the *B. napus* genome in 6 copies, the *FCA* gene is present twice, on only one pair of chromosomes. An *FCA* homologue from *Brassica napus* has  
20 been isolated and sequenced and shows 86.1% average nucleotide sequence homology within the exons, 65.8% within introns and 78% identity at the amino acid level (87% similarity). This *Brassica* gene fully complements a mutation in the *Arabidopsis FCA* gene and can thus be  
25 considered as a fully functional homologue. Homologues have also been detected by Southern blot analysis from *Antirrhinum*, tobacco, sugarbeet, tomato, pea, wheat, maize, rice, rye, *Lolium* and oats.

The *Brassica* FCA homologue whose nucleotide sequence is given in Figure 8a, including the coding sequence, and whose amino acid sequence encoded by the sequence of Figure 8a is shown in Figure 8b, represents and provides further aspects of the present invention in accordance with those disclosed for the *Arabidopsis* FCA gene. For example, mutants, alleles and variants are included, e.g. having at least 80% identity with the sequence of Figure 8b, though high levels of amino acid identity may be limited to functionally significant domains or regions as discussed.

The present invention also extends to nucleic acid encoding an FCA homologue obtained using a nucleotide sequence derived from that shown in Figure 1, or the amino acid sequence shown in Figure 2. Preferably, the nucleotide sequence and/or amino acid sequence shares homology with the sequence encoded by the nucleotide sequence of Figure 1, preferably at least about 50%, or at least about 60%, or at least about 70%, or at least about 75%, or at least about 78%, or at least about 80% homology, most preferably at least about 90% homology, from species other than *Arabidopsis thaliana* and the encoded polypeptide shares a phenotype with the *Arabidopsis thaliana* FCA gene, preferably the ability to influence timing of flowering. These may promote or delay flowering compared with *Arabidopsis thaliana* FCA and mutants, variants or alleles may promote or delay

flowering compared with wild-type. "Homology" may be used to refer to identity.

In certain embodiments, an allele, variant, derivative, mutant or homologue of the specific sequence  
5 may show little overall homology, say about 20%, or about 25%, or about 30%, or about 35%, or about 40% or about 45%, with the specific sequence. However, in functionally significant domains or regions the amino acid homology may be much higher. Comparison of the  
10 amino acid sequences of the FCA polypeptides of the *Arabidopsis thaliana* and *Brassic napus* genes, as in Figure 9, reveals domains and regions with functional significance, i.e. a role in influencing a flowering characteristic of a plant, such as timing of flowering.  
15 Deletion mutagenesis, for example, may be used to test the function of a region of the polypeptide and its role in or necessity for influence of flowering timing.

The nucleotide sequence information provided herein, or any part thereof, may be used in a data-base search to  
20 find homologous sequences, expression products of which can be tested for ability to influence a flowering characteristic. These may have FCA function or the ability to complement a mutant phenotype, which phenotype is delayed flowering, where the delay can be reversed by  
25 a vernalization treatment.

Vernalization is well known in the art and appropriate conditions are at the disposal of skilled artisans. Plants may be vernalized at the seed stage,



immediately after sowing. It may be carried out for 8 weeks, in an 8 hour photoperiod (e.g fluorescent light, PAR  $9.5\text{mmol m}^{-2}\text{s}^{-1}$ , R/FR ratio 3.9) at a temperature of  $5^{\circ}\text{C} \pm 1^{\circ}\text{C}$ .

5           In public sequence databases we recently identified several *Arabidopsis* cDNA clone sequences that were obtained in random sequencing programmes and share homology with *FCA* within both the RRM domains and in the C-terminal regions. BLAST and FASTA searches of databases  
10   have identified 23 *Arabidopsis* expressed sequence tags (ESTs) identified. These clones have been obtained and used in low stringency hybridization experiments with different regions of the *FCA* gene (central and 3'). Eight clones show good homology to the 3' part of the *FCA* gene,  
15   two clones show good homology to the central part and one clone shows good homology to both (42 A 4 - another RNA-binding protein). Similarly, among randomly sequenced rice cDNAs we have identified 10 rice ESTs. These hybridise to *FCA* genomic and cDNA clones under low  
20   stringency conditions. Five clones show good hybridization to *FCA*, particularly C1480.

          By sequencing homologues, studying their expression patterns and examining the effect of altering their expression, genes carrying out a similar function to *FCA*  
25   in regulating flowering time are obtainable. Of course, mutants, variants and alleles of these sequences are included within the scope of the present invention in the

same terms as discussed above for the *Arabidopsis thaliana* FCA gene.

The high level of homology between the FCA genes of *Arabidopsis thaliana* and *Brassica napus*, as disclosed  
5 herein, may also be exploited in the identification of further homologues, for example using oligonucleotides (e.g. a degenerate pool) designed on the basis of sequence conservation.

According to a further aspect, the present invention  
10 provides a method of identifying or a method of cloning a FCA homologue from a species other than *Arabidopsis thaliana*, the method employing a nucleotide sequence derived from that shown in Figure 1 or that shown in Figure 8a. For instance, such a method may employ an  
15 oligonucleotide or oligonucleotides which comprises or comprise a sequence or sequences that are conserved between the sequences of Figures 1 and 8a to search for homologues. Thus, a method of obtaining nucleic acid whose expression is able to influence a flowering  
20 characteristic of a plant is provided, comprising hybridisation of an oligonucleotide or a nucleic acid molecule comprising such an oligonucleotide to target/candidate nucleic acid. Target or candidate nucleic acid may, for example, comprise a genomic or cDNA  
25 library obtainable from an organism known to contain or suspected of containing such nucleic acid. Successful hybridisation may be identified and target/candidate.

nucleic acid isolated for further investigation and/or use.

Hybridisation may involve probing nucleic acid and identifying positive hybridisation under suitably stringent conditions (in accordance with known techniques) and/or use of oligonucleotides as primers in a method of nucleic acid amplification, such as PCR. For probing, preferred conditions are those which are stringent enough for there to be a simple pattern with a small number of hybridisations identified as positive which can be investigated further. It is well known in the art to increase stringency of hybridisation gradually until only a few positive clones remain.

As an alternative to probing, though still employing nucleic acid hybridisation, oligonucleotides designed to amplify DNA sequences may be used in PCR reactions or other methods involving amplification of nucleic acid, using routine procedures. See for instance "PCR protocols; A Guide to Methods and Applications", Eds. Innis et al, 1990, Academic Press, New York.

Preferred amino acid sequences suitable for use in the design of probes or PCR primers are sequences conserved (completely, substantially or partly) between at least two FCA polypeptides able to influence a flowering characteristic, such as timing of flowering, e.g. with the amino acid sequences of Figures 2 and 8b herein.

On the basis of amino acid sequence information oligonucleotide probes or primers may be designed, taking into account the degeneracy of the genetic code, and, where appropriate, codon usage of the organism from the  
5 candidate nucleic acid is derived.

Preferably an oligonucleotide in accordance with the invention, e.g. for use in nucleic acid amplification, has about 10 or fewer codons (e.g. 6, 7 or 8), i.e. is about 30 or fewer nucleotides in length (e.g. 18, 21 or  
10 24).

Assessment of whether or not such a PCR product corresponds to resistance genes may be conducted in various ways. A PCR band from such a reaction might contain a complex mix of products. Individual products  
15 may be cloned and each one individually screened. It may be analysed by transformation to assess function on introduction into a plant of interest.

Generally, nucleic acid according to the invention may comprise a nucleotide sequence encoding a polypeptide  
20 able to complement a mutant phenotype which is delayed in flowering, where that delay can be corrected by a vernalization treatment. Also the present invention provides nucleic acid comprising a nucleotide sequence which is a mutant or variant of a wild-type gene encoding  
25 a polypeptide with ability to influence the timing of flowering, the mutant or variant phenotype being delayed in flowering with the timing of flowering being corrected by vernalization. These are distinguished from the CO

gene reported by Putterill et al 1995, Putterill et al 1993 and the *LD* gene reported by Lee et al 1994. *LD* shows similar characteristics to the *FCA* gene in that a mutation in the gene confers late flowering that is corrected by a vernalization treatment, but *LD* requires a second gene product to influence flowering time in the *Arabidopsis thaliana* Landsberg erecta ecotype (Lee et al 1994, Koornneef et al 1994). Thus in many plant species manipulation of the *LD* gene alone may not influence flowering time. The action of *FCA* is opposite in action to that of phytochromeB, in that mutations in *PHYB* (*hy3*) confer early flowering and introduction of an intact *PHYB* gene into *hy3* mutants restores normal flowering time (Westerl et al 1994). *LD* and *CO* are excluded from the ambit of the present invention. *FCA* and mutants, variants and alleles thereof may not complement an *LD* mutation. *LD* and mutants, variants and alleles thereof may not complement an *FCA* mutation.

The *FCA* amino acid sequence is totally different from those of *CO* and *LD*.

The action of *FCA* can also be distinguished from ectopic expression of meristem identity or MADS box genes that alter flowering time (Weigel and Nilsson 1995, Chung et al 1994, Mandel and Yanofsky 1995, Mizukama and Ma 1992). Apart from an early flowering phenotype, ectopic or overexpression of meristem identity or MADS box genes produces many additional perturbations to both the

vegetative and floral phenotype of the plant (eg. short stature, reduced apical dominance, sterile flowers).

Also according to the invention there is provided a plant cell having incorporated into its genome a sequence  
5 of nucleotides where different introns have been removed. A further aspect of the present invention provides a method of making such a plant cell involving introduction of a vector comprising the sequence of nucleotides into a plant cell and causing or allowing recombination between  
10 the vector and the plant cell genome to introduce the sequence of nucleotides into the genome.

Plants which comprise a plant cell according to the invention are also provided, along with any part or propagule thereof, seed, selfed or hybrid progeny and  
15 descendants and any part or propagate thereof.

The invention further provides a method of influencing the flowering characteristics of a plant comprising expression of a heterologous *FCA* gene sequence (or mutant, allele, variant or homologue thereof, as  
20 discussed) within cells of the plant. The term "heterologous" indicates that the gene/sequence of nucleotides in question have been introduced into said cells of the plant or an ancestor thereof, using genetic engineering, ie by human intervention. The gene may be on  
25 an extra-genomic vector or incorporated, preferably stably, into the genome. The heterologous gene may replace an endogenous equivalent gene, ie one which normally performs the same or a similar function in

control of flowering, or the inserted sequence may be additional to the endogenous gene. An advantage of introduction of a heterologous gene is the ability to place expression of the gene under the control of a promoter of choice, in order to be able to influence gene expression, and therefore flowering, according to preference. Furthermore, mutants and variants of the wild-type gene, eg with higher or lower activity than wild-type, may be used in place of the endogenous gene.

10       The principal flowering characteristic which may be altered using the present invention is the timing of flowering. Under-expression of the gene product of the *FCA* gene leads to delayed flowering (as indicated by the *fca* mutant phenotype and Example 3, antisense  
15 experiments) that can be overcome to early flowering by a vernalization treatment; over-expression may lead to earlier flowering (Examples 2, 4 and 5). This degree of control is useful to ensure synchronous flowering of male and female parent lines in hybrid production, for  
20 example. Another use is to advance or retard the flowering in accordance with the dictates of the climate so as to extend or reduce the growing season. This may involve use of anti-sense or sense regulation.

25       The nucleic acid according to the invention, such as a *FCA* gene or homologue, may be placed under the control of an externally inducible gene promoter thus placing the timing of flowering under the control of the user. This is advantageous in that flower production, and subsequent

events such as seed set, may be timed to meet market demands, for example, in cut flowers or decorative flowering pot plants. Delaying flowering in pot plants is advantageous to lengthen the period available for transport of the product from the producer to the point of sale and lengthening of the flowering period is an obvious advantage to the purchaser.

In a further aspect the present invention provides a gene construct comprising an inducible promoter operatively linked to a nucleotide sequence provided by the present invention, such as the *FCA* gene or *Arabidopsis thaliana*, a homologue from another plant species, e.g. a *Brassica* such as *Brassica napus*, or any mutant, variant or allele thereof. As discussed, this enables control of expression of the gene. The invention also provides plants transformed with said gene construct and methods comprising introduction of such a construct into a plant cell and/or induction of expression of a construct within a plant cell, by application of a suitable stimulus, an effective exogenous inducer.

The term "inducible" as applied to a promoter is well understood by those skilled in the art. In essence, expression under the control of an inducible promoter is "switched on" or increased in response to an applied stimulus. The nature of the stimulus varies between promoters. Some inducible promoters cause little or undetectable levels of expression (or no expression) in the absence of the appropriate stimulus. Other inducible



promoters cause detectable constitutive expression in the absence of the stimulus. Whatever the level of expression is in the absence of the stimulus, expression from any inducible promoter is increased in the presence of the correct stimulus. The preferable situation is where the level of expression increases upon application of the relevant stimulus by an amount effective to alter a phenotypic characteristic. Thus an inducible (or "switchable") promoter may be used which causes a basic level of expression in the absence of the stimulus which level is too low to bring about a desired phenotype (and may in fact be zero). Upon application of the stimulus, expression is increased (or switched on) to a level which brings about the desired phenotype.

Suitable promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) gene promoter that is expressed at a high level in virtually all plant tissues (Benfey et al, 1990a and 1990b); the cauliflower meri 5 promoter that is expressed in the vegetative apical meristem as well as several well localised positions in the plant body, eg inner phloem, flower primordia, branching points in root and shoot (Medford, 1992; Medford et al, 1991) and the *Arabidopsis thaliana* LEAFY promoter that is expressed very early in flower development (Weigel et al, 1992).

When introducing a chosen gene construct into a cell, certain considerations must be taken into account, well known to those skilled in the art. The nucleic acid to be inserted should be assembled within a construct

which contains effective regulatory elements which will drive transcription. There must be available a method of transporting the construct into the cell. Once the construct is within the cell membrane, integration into the endogenous chromosomal material either will or will not occur. Finally, as far as plants are concerned the target cell type must be such that cells can be regenerated into whole plants.

Plants transformed with the DNA segment containing the sequence may be produced by standard techniques which are already known for the genetic manipulation of plants. DNA can be transformed into plant cells using any suitable technology, such as a disarmed Ti-plasmid vector carried by *Agrobacterium* exploiting its natural gene transfer ability (EP-A-270355, EP-A-0116718, NAR 12(22) 8711 - 87215 1984), particle or microprojectile bombardment (US 5100792, EP-A-444882, EP-A-434616) microinjection (WO 92/09696, WO 94/00583, EP 331083, EP 175966), electroporation (EP 290395, WO 8706614) or other forms of direct DNA uptake (DE 4005152, WO 9012096, US 4684611). *Agrobacterium* transformation is widely used by those skilled in the art to transform dicotyledonous species. Although *Agrobacterium* has been reported to be able to transform foreign DNA into some monocotyledonous species (WO 92/14828), microprojectile bombardment, electroporation and direct DNA uptake are preferred where *Agrobacterium* is inefficient or ineffective. Alternatively, a combination of different techniques may

be employed to enhance the efficiency of the transformation process, eg bombardment with Agrobacterium coated microparticles (EP-A-486234) or microprojectile bombardment to induce wounding followed by co-cultivation  
5 with Agrobacterium (EP-A-486233).

The particular choice of a transformation technology will be determined by its efficiency to transform certain plant species as well as the experience and preference of the person practising the invention with a particular  
10 methodology of choice. It will be apparent to the skilled person that the particular choice of a transformation system to introduce nucleic acid into plant cells is not essential to or a limitation of the invention.

In the present invention, over-expression may be  
15 achieved by introduction of the nucleotide sequence in a sense orientation. Thus, the present invention provides a method of influencing a flowering characteristic of a plant, the method comprising causing or allowing expression of the polypeptide encoded by the nucleotide  
20 sequence of nucleic acid according to the invention from that nucleic acid within cells of the plant.

Under-expression of the gene product polypeptide may be achieved using anti-sense technology or "sense regulation".

25 The use of anti-sense genes or partial gene sequences to down-regulate gene expression is now well-established. Double-stranded DNA is placed under the control of a promoter in a "reverse orientation" such

that transcription of the "anti-sense" strand of the DNA yields RNA which is complementary to normal mRNA transcribed from the "sense" strand of the target gene. The complementary anti-sense RNA sequence is thought then to bind with mRNA to form a duplex, inhibiting translation of the endogenous mRNA from the target gene into protein. Whether or not this is the actual mode of action is still uncertain. However, it is established fact that the technique works. See, for example, Rothstein et al, 1987; Smith et al, 1988; Zhang et al, 1992, English et al 1996. The complete sequence corresponding to the coding sequence in reverse orientation need not be used. For example fragments of sufficient length may be used. It is a routine matter for the person skilled in the art to screen fragments of various sizes and from various parts of the coding sequence to optimise the level of anti-sense inhibition. It may be advantageous to include the initiating methionine ATG codon, and perhaps one or more nucleotides upstream of the initiating codon. A suitable fragment may have about 14-23 nucleotides, e.g. about 15, 16 or 17.

Anti-sense regulation may itself be regulated by employing an inducible promoter in an appropriate construct.

Thus, the present invention also provides a method of influencing a flowering characteristic of a plant, the method comprising causing or allowing anti-sense

transcription from nucleic acid according to the invention within cells of the plant.

When additional copies of the target gene are inserted in sense, that is the same, orientation as the target gene, a range of phenotypes is produced which includes individuals where over-expression occurs and some where under-expression of protein from the target gene occurs. When the inserted gene is only part of the endogenous gene the number of under-expressing individuals in the transgenic population increases. The mechanism by which sense regulation occurs, particularly down-regulation, is not well-understood. However, this technique is also well-reported in scientific and patent literature and is used routinely for gene control. See, for example, van der Krol, 1990; Napoli et al, 1990; Zhang et al, 1992.

Thus, the present invention also provides a method of influencing a flowering characteristic of a plant, the method comprising causing or allowing expression from nucleic acid according to the invention within cells of the plant to suppress activity of a polypeptide with ability to influence a flowering characteristic. Here the activity of the polypeptide is preferably suppressed as a result of under-expression within the plant cells.

Modified version of FCA may be used in influencing a flowering characteristic of a plant. For example a mutant identified herein as *fca-1*, *fca-3* or *fca-4* may be

employed. The sequence changes resulting in these mutants and the resulting phenotypes are discussed above.

*Promotion of FCA activity to cause early flowering*

- 5           Mutations that reduce *FCA* activity cause late flowering under both long and short day conditions, indicating *FCA* involvement in promoting flowering constitutively. Double mutant experiments have also indicated that *FCA* function may be required both upstream and downstream of the gene products involved in conferring inflorescence/floral meristem identity eg. *LEAFY*, *APETALA1* and *TERMINAL FLOWER*. Thus *FCA* function may be involved in the ability of meristems to respond to *LEAFY*, *APETALA1* and *TERMINAL FLOWER* gene products.
- 10
- 15           The fully spliced *FCA* transcript is present at very low abundance in all conditions so far analysed. Although the *fca* mutation is recessive transgenic *fca* plants homozygous for an introduced wild-type *FCA* gene flowered slightly earlier than plants carry one copy (Example 2), suggesting that under some conditions the level of the *FCA* transcript is limiting to flowering time. This indicates that flowering may be manipulated by using foreign promoters to alter the expression of the gene. In addition, the majority of the transcript is present in a form that cannot make active protein. Thus alternative splicing may be a specific control mechanism to maintain relatively low levels of the *FCA* protein. Alteration of this splicing pattern, for example by introducing an *FCA*
- 20
- 25

gene lacking introns into plants, may give much higher levels of the FCA protein which in turn would give accelerated flowering.

5     *Causing early flowering under non-inductive or inductive conditions*

Wild-type *Arabidopsis* plants flower extremely quickly under inductive conditions and the FCA gene is expressed prior to flowering, although at a low level.

10    The level of the FCA product may be increased by introduction of promoter, eg CaMV35S or meri 5, fusions. In addition, introduction of an FCA gene lacking introns may increase the level of FCA protein and cause early flowering in all conditions.

15

*Inhibition of FCA activity to cause late flowering*

*fca* mutations cause late flowering of *Arabidopsis*.

Transgenic approaches may be used to reduce FCA activity and thereby delay or prevent flowering in a range of

20    plant species. A variety of strategies may be employed.

This late flowering can then be overcome, if so desired, by giving the imbibed seed or plants of different ages, a vernalization treatment.

25    *Expression of sense or anti-sense RNAs*

In several cases the activity of endogenous plant genes has been reduced by the expression of homologous antisense RNA from a transgene, as discussed above.

Similarly, the expression of sense transcripts from a transgene may reduce the activity of the corresponding endogenous copy of the gene, as discussed above.

Expression of an antisense transcript from the *FCA* gene  
5 has been shown reduce activity of the endogenous gene and cause late flowering (Example 3).

*Expression of modified versions of the FCA protein*

RNA binding proteins have a modular structure in  
10 which amino acid sequences required for binding different RNA molecules are separate domains of the protein (Burd and Dreyfuss 1994). This permits the construction of truncated or fusion proteins that display only one of the functions of the RNA binding protein. In the case of *FCA*,  
15 modification of the gene in vitro and expression of modified versions of the protein may lead to dominant inhibition of the endogenous, intact protein and thereby delay flowering. This may be accomplished in various ways, including the following:

20

*Expression of a truncated FCA protein.*

Some multi-RNP motif proteins can bind different RNA sequences simultaneously. U1 A for example, binds to U1 small nuclear RNA through its first RNA-binding domain  
25 and to pre-mRNA sequences through its second, thus controlling splicing (Burd and Dreyfuss 1994). Expression of an *FCA* protein with only one of these RNP motifs may dominantly block *FCA* action, by preventing binding of the



full size FCA protein. Also expression of a mutant FCA protein not encoding the C terminal sequences may prevent the correct alignment of the binding of the RNA molecule and so again block wild-type FCA binding.

5

Aspects and embodiments of the present invention will now be illustrated, by way of example, with reference to the accompanying figures. Further aspects and embodiments will be apparent to those skilled in the art. All documents mentioned in this text are incorporated herein by reference.

In the Figures:

Figure 1 shows a nucleotide sequence according to one embodiment of the invention, being the sequence of the genomic region encoding FCA obtained from *Arabidopsis thaliana*. Introns are shown in small letters, exons in capitals. Features: ▼(1118) - transcription start; □(1532-1534, 1568-70, 1601-1603) - putative translation start ATG; ⌈β(2753) - Poly A site of β-transcript; ≡(7056-7377) - alternative splicing around intron II; \_\_ (8771-73) - translation stop TAA; ⌈(9256) - Poly A site. Additional translational stop codon at 3026-3028 within intron 3.

Figure 2 shows the predicted amino acid sequence derived from the nucleotide sequence encoding the FCA ORF.

Figure 3 shows the nucleotide sequence of the *FCA*  $\alpha_B$  gene, including 5' and 3' flanking sequences. The sequence within the ORF is that of one of the abundant transcripts, that is 18 introns have been spliced out but  
5 intron 3 remains. The position of termination of the other abundant transcript is indicated. Primer sequences are given in Table 2. Restriction sites: *Sal*I - 352; *Hind*III - 776; *Xba*I - 1157; *Hind*III - 3125; *Bgl*II - 3177; *Cla*I - 3293; *Bam*HI - 3549; *Hind*III - 4728; *Spe*I - 5003.  
10 Other important landmarks: 1293-poly A tail added after this nucleotide in cDNA clone 77B or *FCA* transcript  $\alpha$ ; 897-5' splice site of intron 3: 2973 3' splice site of intron 3.

Figure 4 compares the *FCA* RRM motifs with those from  
15 the *Drosophila* *SEX-LETHAL* and *TRA-2* genes. Also shown are the C-terminal amino acids with homology to yeast and *C. elegans* proteins.

Figure 5 shows the recombination analysis to position the *FCA* gene.

20 Figure 6 shows the complementation analysis to localize the *FCA* gene.

Figure 7 shows the complexity and position of the *FCA* gene on the complementing cosmids.

Figure 8 shows the nucleotide sequence of the  
25 *Brassica napus* *FCA* homologue and encoded polypeptide: Figure 8a - *Brassica* *FCA* nucleotide sequence including coding sequence; Figure 8b - polypeptide amino acid sequence encoded by coding sequence of Figure 8a.

Figure 9 shows an alignment of the *Arabidopsis* and *Brassica* FCA amino acid sequences. Topline is *Arabidopsis*; bottom line is *Brassica*.

Figure 10 shows the different transcripts produced from the FCA gene. — open reading frame; \* conserved region in *C. elegans* and yeast ESTs; R1, R2 RNA-binding domains 1 and 2.

#### EXAMPLE 1 - CLONING AND ANALYSIS OF THE FCA GENE

10 Identification of a 300kb genomic region carrying the FCA gene of *Arabidopsis thaliana*.

The *fca* mutation had been mapped relative to visible markers to 29cM on chromosome 4. In order to map the locus relative to molecular markers as a starting point for cloning by chromosome walking, the segregation pattern of RFLP markers mapping to the top half of chromosome 4 was analysed in 171 late (homozygous recessive class) flowering individuals from the F2 of a cross between the late flowering mutant *fca-1* (in a Landsberg erecta background) and the polymorphic early flowering ecotype Columbia. This analysis positioned the FCA locus in a 5.2cM interval between markers m326 and m226.

These markers were then used as the starting points for the chromosome walk. YAC clones containing these RFLP markers were identified by colony hybridization experiments. In the initial experiments, the YAC libraries used were the EG, EW and ABI libraries but as

another became available (yUP-May1992) they were incorporated into the analysis. Positively hybridizing YAC clones were confirmed using Southern blot analysis. They were sized using PFGE and Southern blot analysis and  
5 then end-probes were generated using either inverse PCR or left-end rescue for use in chromosome walking experiments. In the majority of cases, each step in the walk was covered by two independent YAC clones to avoid false linkages generated by chimaeric YAC clones. These  
10 constituted a significant fraction of the EG, EW and yUP libraries and complicated the assembly of the YAC contig. The result of the generation and analysis of 65 end-probes was a YAC contig covering the m326-m226 interval that included 57 YAC clones.

15 Polymorphisms between Landsberg erecta and Columbia were determined for the left end-probe of EG9D2, right end-probe of YAC clone yUP13C7, right end-probe of YAC clone yUP3F7 and right end-probe of YAC clone EW20B3. Analysis of the segregation pattern of these markers on  
20 pooled progeny of recombinants with cross-over points mapping in the m326-m226 interval defined the region carrying the FCA gene to between the polymorphisms identified by yUP3F7RE and m226. This interval was covered by two overlapping YAC clones EW20B3 and  
25 ABI10C10.

In order to further define the position of the FCA gene, more probes were required that mapped within the two overlapping YAC clones. This was achieved by using

end-probes from YAC clones ABI3C4, ABI6C3, a random Sau3A fragment from YAC clone EW20B3 (W5) and two cosmids cAtA2 and g19247. Restriction maps for SmaI, MluI and PacI were constructed and used to position the probes within the YAC clones.

Additional recombinants, where the cross-over point mapped close to the FCA locus, were generated by selecting individual plants that were arabinose resistant and had an early/intermediate flowering from the F2 generation of a cross between *fca* (in Landsberg erecta) and *ara1* (in Columbia). Progeny of these were checked to confirm that they were homozygous for the arabinose resistance allele and heterozygous for the *fca* mutation. Three of these individuals (A2/7, A1/8 and A4/7) were analysed with the RFLP markers 3F7RE, W5, cAtA2, 19247, 3C4LE, 6C3LE and 226. This defined the north end of the genomic region carrying the FCA gene as within the cosmids cAtA2 and 19247. This information is summarized in Fig.5.

#### Complementation analysis to define the FCA gene.

The two YAC clones EW20B3 and ABI10C10 were gel-purified and hybridized to filters carrying 25500 cosmid clones that contained 15-20kb of *Arabidopsis thaliana* Landsberg erecta genomic DNA. This cosmid library was constructed in a new vector (04541) by cloning a 1.6kb BglII fragment from pHC79 carrying the lambda cos fragment into in the vector pSLJ1711. The resulting

highly stable cosmid cloning vehicle carries  
Agrobacterium border sequences for transfer of DNA into  
plant chromosomes, a 35S-NPTII plant selectable marker,  
lacZ-lacI sequences for the blue/white insert selection  
5 in E.coli and a polylinker with 7 cloning sites.

Positively hybridizing colonies were analysed by  
hybridizing each clone to Southern blots carrying all the  
cosmid clones digested with a HindIII, EcoRI and BamHI.  
This generated a restriction map for the insert of each  
10 cosmid and indicated which clones carried overlapping  
inserts. The cosmids were also run alongside plant DNA  
and hybridized with the cosmid to confirm that the cosmid  
insert was colinear with the plant DNA. The two cosmid  
clones, cAtA2 and cAtB1, mapping to this interval were  
15 isolated from a different cosmid library (Olszewski and  
Ausubel 1988). The result of this analysis was a cosmid  
contig covering the 300kb interval in which the FCA locus  
had been defined.

Six mutant *fca* alleles were available, two of which  
20 had been generated by FN irradiation and one by X-ray  
irradiation. Irradiation-induced mutations are frequently  
associated with genomic rearrangements or deletions. In  
case this would further refine the location of the FCA  
gene, the genomic region covered by the YAC clones EW20B3  
25 and ABI10C10 was examined in all six alleles. The two YAC  
clones were hybridized to PFGE Southern blots carrying  
DNA from the different alleles digested with SmaI and  
MluI. A ~50kb MluI fragment was found to be slightly

smaller in the *fca-4* allele. Further analysis by hybridization of cosmid clones, corresponding to the region showing the difference, indicated that part of the alteration had occurred in a 1.9kb BamHI fragment carried  
5 in cosmids cAtA2 and 19247. This focused our efforts in the first complementation experiments to cosmid clones at the north end of the contig.

Eleven cosmid clones shown in Fig 6, starting with those at the left end, were introduced into the  
10 *Arabidopsis fca-1* mutant using the root explant transformation procedure (Valvekens et al 1988). Seed were collected from self-fertilized kanamycin resistant individuals and analysed with respect to their kanamycin segregation and flowering time. The number of  
15 transformants showing complementation to early flowering for each cosmid is shown in Figure 6. The four cosmids that resulted in complementation mapped to the end of the genomic region where the inversion in the *fca-4* allele mapped.

20

#### *Identification of the FCA gene.*

The complete genomic sequence of Columbia allele corresponding to the genomic region within the complementing cosmid clones was obtained through the  
25 efforts of the *Arabidopsis* sequencing initiative centred within this department (G. Murphy pers. comm.). The majority of the genomic region contained in the complementing cosmids is carried on three BamHI

restriction fragments, 4, 1.9 and 2kb. These were isolated and hybridized either separately or pooled to  $1 \times 10^6$  phage clones of the PRL-2 cDNA library. This library had been made from pooled RNA samples and was made available by Tom Newman (Michigan). Four clones hybridizing to the 2kb BamHI fragment and 3 to the 4 and 1.9kb fragments were isolated and characterized. They identified two cDNA clones with insert sizes ~1700bp and 1350bp. Analysis of the sizes of the transcripts hybridizing to these two cDNA clones showed that one (in *fca-4*) was reduced in size relative to the other alleles and wild-type and so this cDNA clone was assigned to the *FCA* gene. The other clone showed no differences and was termed 77B

The transcript size of the putative *FCA* gene was >3kb indicating that the cDNA clone was not full length. The cDNA clone was sequenced and found to encode an insert of 1811bp. Primers were designed from the genomic sequence (marked BamX primer on Figure 3) and the 5' end of the cDNA sequence (marked IanRT1 and IanRT2 on Figure 3). First strand cDNA was made using the IanRT2 primer to prime RNA isolated from wild-type seedlings (2 leaf stage). This was used with primers BamX and IanRT2 to PCR amplify a fragment detected as a faint band on an ethidium bromide stained gel. The PCR product was diluted 1/300 and reamplified using primers BamX and IanRT1. The product from this reaction was end-filled using T4 DNA polymerase and cloned into the EcoRV site of the general



cloning vector Bluescript KSII (Stratagene). The product was sequenced and found to be colinear with the genomic sequence and extend the sequence of the cDNA clone by 735bp.

5           The sequence was compared to all available sequences using BlastX, BlastN and TblastN. Significant homologies were detected in the TblastN search to a class of proteins previously defined as RNA binding proteins. The characteristic of these proteins is the presence of one  
10 or more RRM motifs made up of conserved amino acids covering an 80 amino acid region (shown in Fig. 4). The positioning of sub-motifs RNP2 and RNP1 and individual conserved amino acids is always maintained within the whole RRM motif. Translation of the sequence of the FCA  
15 cDNA clone extended in the RT-PCR experiments showed the presence of multiple translation stop codons in the 5' region of the sequence. The first methionine residue downstream of the last translation stop codon and in frame with the rest of the FCA protein was located in the  
20 middle of the RRM motif, splitting RNP2 and RNP1. The strong homology of the RRM motif to other RNA binding proteins suggested that this MET residue was not the beginning of the FCA protein. In addition, the transcripts of a large number of RNA-binding proteins are  
25 alternatively spliced to yield active and inactive products. The splicing is then regulated, often in an autoregulatory fashion, to control the production of the active protein. These facts suggested that the FCA

transcript generated in the RT-PCR experiments contained an intron, just upstream of the RRM motif.

In order to test this hypothesis, several primers were designed from the genomic sequence for use in further RT-PCR experiments. First strand cDNA was made from RNA isolated from seedlings (4 leaf stage), primed with random hexamers (Boehringer). Primers lying within the sequence 5' to the FCA cDNA up to the 3' end of the 77B cDNA (the other cDNA clone hybridizing to the complementing cosmid clones), together with IanRT1 gave amplification products of the expected size from the genomic sequence but did not yield smaller products as would be expected from a transcript in which an intervening intron had been spliced out. A primer lying within the 77B cDNA clone marked as cDNAII-BamHI (in Fig.3) was then used in conjunction with the IanRT1 primer. No band was visible on an ethidium bromide stained agarose gel after 30 cycles of amplification. The PCR reaction was then diluted 1/300 and re-amplified using primers cDNAII-1 and RevEx4 (shown in Figure 3). The PCR product was digested with SalI and BglII restriction enzymes and cloned into SalI and BamHI digested BluescriptKSII plasmid. Sequence analysis of the 760bp product and comparison to the genomic sequence revealed that a 2kb intron had been spliced out to join the ORF within the 77B cDNA to that carrying the RRM motif in the FCA gene. This splicing revealed the

presence of a second intact RRM motif interrupted by intron 3.

Direct comparison of the *FCA* sequence with that of *LUMINIDEPENDENS* and *CO*, the other flowering time genes  
5 cloned from *Arabidopsis* (Lee et al, 1994, Putterill et al 1995), detected no significant homology.

#### *Mutations in the fca mutant alleles.*

cDNA was made from RNA isolated from the mutant  
10 alleles. This was amplified using cDNAII-BamHI and cDNA-3'a: BamX and IanRT1; fca5'-1 and fca3'-a (positions indicated on Fig 3). The resulting PCR fragments were cloned and sequenced and compared to the sequence of the wild-type Landsberg erecta transcript. The *fca-1* mutation  
15 converted a C nucleotide at position 6861 into a T. Thus a glutamine codon (CAA) is changed into a stop codon (TAA). The *fca-3* mutation converted a G nucleotide at position 5271 into an A. The effect of this mutation is to alter the 3' splice junction of intron 7 such that a  
20 new 3' splice junction is used 28 nucleotides into exon 8. The *fca-4* mutation is the result of a rearrangement with the break-point at position 4570 (within intron 4).

#### EXAMPLE 2 - ISOLATION AND SEQUENCE ANALYSIS OF THE 25 *BRASSICA NAPUS* HOMOLOGUE.

A *Brassica napus* genomic library constructed from Sau3A partially digested DNA cloned into lambda DASH<sup>RII</sup>/BamHI vector (Stratagene) was obtained. The

library was screened using the 1811bp *FCA* cDNA clone. A clone carrying a 12kb insert was isolated which hybridized to the *FCA* cDNA clone and the 77B cDNA clone. The lambda clone was digested with *SalI* which released  
5 the full length 12kb *Brassica* insert and this was cloned into Bluescript KSII. Restriction fragments of this clone (a combination of *EcoRI*, *SacI* and *BamHI*) were subcloned into BluescriptKSII and sequenced.

The 12kb *Brassica* fragment was also subcloned into  
10 the *XhoI* restriction site of the *Agrobacterium* binary vector pSLJ1714 (Jones et al 1992), for transformation into the *fca* mutant. When introduced into the *fca*-4 mutation, using root explant transformation, progeny of the transformant segregated early flowering plants. These  
15 flowered with a mean of 8.3 leaves compared to wild-type Landsberg erecta grown alongside with 9.1 leaves and *fca*-4 with 24.1 leaves. Thus the *Brassica FCA* gene fully complements the *fca*-4 mutation.

## 20 *Expression of FCA mRNA*

PolyA mRNA was isolated from a range of developmental stages: 2 leaf, 4 leaf, 6 leaf and 10 leaf, roots and inflorescences, fractionated on Northern blots and hybridized with the 1811bp *FCA* cDNA clone. The  
25 combined *FCA* transcript  $\gamma$  was present at approximately the same amount in all tissues examined except for the inflorescences where expression was slightly lower. The prematurely polyadenylated transcript  $\beta$  was detected

using 77B cDNA clone as a probe. The  $\beta$  transcript was ~20-fold more abundant than  $\gamma_A + B$ . Transcripts  $\alpha_A + B$  containing intron 3 were not detected on a northern blot and could only be found using RT-PCR.

5 FCA expression has also been analysed using RNase protection assays. Using a probe (725 bp to 1047 bp from  $\gamma_B$  construct) the  $\gamma_A + B$  transcripts were detected at similar levels in a range of developmental stages in both long and short day photoperiods, and at lower levels in  
10 rosettes and inflorescences of mature plants. The  $\beta$  transcript was at a higher level in these tissues consistent with the northern blot analysis.

#### METHODS FOR EXAMPLES 1 AND 2

##### 15 *Growth conditions and measurement of flowering time*

Flowering time was measured under defined conditions by growing plants in Sanyo Gallenkamp Controlled Environment rooms at 20°C. Short days comprised a photoperiod of 10 hours lit with 400 Watt metal halide  
20 power star lamps supplemented with 100 watt tungsten halide lamps. This provided a level of photosynthetically active radiation (PAR) of 113.7  $\mu$ moles photons  $m^{-2}s^{-1}$  and a red:far red light ratio of 2.41. A similar cabinet and lamps were used for the long day. The photoperiod was for  
25 10 hours under the same conditions used for short days and extended for a further 8 hours using only the tungsten halide lamps. In this cabinet the combination of lamps used for the 10 hour period provided a PAR of 92.9

$\mu$ moles photons  $m^{-2} s^{-1}$  and a red:far red ratio of 1.49. The 8 hour extension produced PAR of 14.27  $\mu$ moles  $m^{-2} s^{-1}$  and a red:far-red ratio of 0.66.

The flowering times of large populations of plants  
5 were measured in both greenhouse and cabinet conditions. Flowering time was measured by counting the number of leaves, excluding the cotyledons, in the rosette and on the inflorescence. Leaf numbers are shown with the standard error at 95% confidence limits. The number of  
10 days from sowing to the appearance of the flower bud was also recorded, but is not shown. The close correlation between leaf number and flowering time was previously demonstrated for Landsberg erecta and *fca* alleles (Koorneef et al, 1991).

15

*Cosmid and RFLP markers.*

DNA of lambda clones m210, m326, m580, m226 were obtained from Elliot Meyerowitz (Caltech, Pasadena). Total DNA was used as radiolabelled probe to YAC library  
20 colony filters and plant genomic DNA blots. Cosmids g10086, g4546, g4108, g19247 were obtained from Brian Hauge and Howard Goodman (MGH, Boston), cultured in the presence of 30 mg/l kanamycin, and maintained as glycerol stocks at - 70°C. Total cosmid DNA was used as  
25 radiolabelled probe to YAC library colony filters and plant genomic DNA blots. Cosmid clones cAtA2 and cATB1 were obtained from Chris Cobbett (University of Melbourne) and cultured in the presence of 10mg/l

tetracycline. Cosmid pCITd23 was provided by Elliot Meyerowitz (Caltech, Pasadena), cultured in the presence of 100 µg/ml streptomycin/spectinomycin and maintained as a glycerol stock at - 70° C. pCIT30 vector sequences share homology to pYAC4 derived vectors, and therefore YAC library colony filters were hybridised with insert DNA extracted from the cosmid. Total DNA of pCITd23 was used as radiolabelled probe to plant genomic DNA blots.

10 *YAC libraries.*

The EG and ABI libraries were obtained from Chris Somerville (Michigan State University). The EW library was obtained from Jeff Dangl (Max Delbruck Laboratory, Cologne) and the yUP library from Joe Ecker (University of Pennsylvania). Master copies of the libraries were stored at -70°C (as described by Schmidt et al. Aust. J. Plant Physiol. 19: 341-351 (1992)). The working stocks were maintained on selective Kiwibrew agar at 4°C. Kiwibrew is a selective, complete minimal medium minus uracil, and containing 11% Casamino acids. Working stocks of the libraries were replated using a 96-prong replicator every 3 months.

*Yeast colony filters.*

25 Hybond-N (Amersham) filters (8cm x 11cm) containing arrays of yeast colony DNA from 8-24 library plates were produced and processed (as described by Coulson et al. Nature 335:184-186 (1988) and modified (as described by

Schmidt and Dean Genome Analysis, vol.4: 71-98 (1992)). Hybridisation and washing conditions were according to the manufacturer's instructions. Radiolabelled probe DNA was prepared by random-hexamer labelling.

5

*Yeast chromosome preparation and fractionation by pulsed field gel electrophoresis (PFGE).*

Five millilitres of Kiwibrew was inoculated with a single yeast colony and cultured at 30°C for 24 h. Yeast spheroplasts were generated by incubation with 2.5mg/ml Novozym (Novo Biolabs) for 1 h at room temperature. Then 1 M sorbitol was added to bring the final volume of spheroplasts to 50 µl. Eighty microlitres of molten LMP agarose (1% InCert agarose, FMC) in 1 M sorbitol was added to the spheroplasts, the mixture was vortexed briefly and pipetted into plug moulds. Plugs were placed into 1.5ml Eppendorf tubes and then incubated in 1 ml of 1 mg/ml Proteinase K (Boehringer Mannheim) in 100 mM EDTA, pH 8, 1% Sarkosyl for 4 h at 50°C. The solution was replaced and the plugs incubated overnight. The plugs were washed three times for 30 min each with TE and twice for 30 min with 0.5 x TVBE. PFGE was carried out using the Pulsaphor system (LKB). One-third of a plug was loaded onto a 1% agarose gel and electrophoresed in 0.5 x TBE at 170 V, 20 s pulse time, for 36 h at 4°C. DNA markers were concatemers of lambda DNA prepared as described by Bancroft and Wolk, Nucleic A Res. 16:7405-7418 (1988). DNA was visualised by staining with ethidium bromide.



*Yeast genomic DNA for restriction enzyme digestion and inverse polymerase chain reaction (IPCR).*

Yeast genomic DNA was prepared essentially as described by Heard et al. (1989) except that yeast spheroplasts were prepared as above. Finally, the DNA was extracted twice with phenol/chloroform, once with chloroform and ethanol precipitated. The yield from a 5ml culture was about 10 $\mu$ g DNA.

10 *Isolation of YAC left-end probes by plasmid rescue.*

Plasmid rescue of YAC left-end fragments from EG, ABI and EW YACs was carried out as described by Schmidt et al. (1992). IPCR was used to generate left and right end fragments using the protocol and primers described in Schmidt et al (1992).

*Gel blotting and hybridisation conditions.*

Gel transfer to Hybond-N, hybridisation and washing conditions were according to the manufacturer's instructions, except that DNA was fixed to the filters by UV Stratalinker treatment and/or baked at 80°C for 2 h. Radiolabelled DNA was prepared by random hexamer labelling.

25 *RFLP analysis.*

Two to three micrograms of plant genomic DNA was prepared from the parental plants used in the crosses and cleaved in a 300  $\mu$ l volume. The digested DNA was ethanol

precipitated and separated on 0.7% agarose gels and blotted onto Hybond-N filters. Radiolabelled cosmid, lambda or YAC end probe DNA was hybridised to the filters to identify RFLPs.

5

#### *RNA extractions*

RNA was extracted using a method described by Dean et al (1985)

polyA RNA was isolated using the polyAtract<sup>R</sup> mRNA

10 isolation system (Promega).

#### *DNA extractions*

*Arabidopsis* DNA was performed by a CTAB extraction method described by Dean et al (1992).

15

#### *Isolation of cDNA by RT-PCR*

Total RNA was isolated from whole seedlings at the 2-3 leaf stage growing under long days in the greenhouse. For first strand cDNA synthesis, 10 µg of RNA in a volume of 10 µl was heated to 65°C for 3 minutes, and then quickly cooled on ice. 10 µl of reaction mix was made containing 1 µl of RNasin, 1 µl of standard dT17-adapter primer (1 µg/µl; Frohman et al, 1988), 4µl of 5x reverse transcriptase buffer (250mM TrisHCl pH8.3, 375mM KCl, 25 15mM MgCl<sub>2</sub>), 2µl DTT (100mM), 1µl dNTP (20mM), 1µl reverse transcriptase (200 units, M-MLV Gibco). This reaction mix was then added to the RNA creating a final

volume of 20 $\mu$ l. The mixture was incubated at 42°C for 2 hours and then diluted to 200  $\mu$ l with water.

10 $\mu$ l of the diluted first strand synthesis reaction was added to 90 $\mu$ l of PCR mix containing 4 $\mu$ l 2.5mM dNTP, 5 10 $\mu$ l 10xPCR buffer (Boehringer plus Mg), 1 $\mu$ l of a 100ng/ $\mu$ l solution of each of the primers, 73.7 $\mu$ l of water and 0.3 $\mu$ l of 5 units/ $\mu$ l Taq polymerase (Boehringer or Cetus Amplitaq). The reaction was performed at 94°C for 1 minute, 34 cycles of 55°C for 1 minute, 72°C for 2 minutes 10 and then finally at 72°C for 10 minutes.

#### *DNA sequencing*

The Sanger method was used to sequence fragments of interest inserted in a Bluescript plasmid vector.

15 Reactions were performed using a Sequenase kit (United States Biochemical Corporation).

#### *Screening the Landsberg erecta cosmid library and the PRL-2 cDNA library.*

20 26000 clones arrayed in microtitre plates were screened by gridding offsets from 16 microtitre plates onto LB-tet (10 $\mu$ g/ml) plates and then taking colony lifts onto Hybond N filters. 1x10<sup>6</sup> plaques of the CD4-71-PRL2 library (supplied by the Arabidopsis Biological Resource 25 Center at Ohio State University) were screened by plating 20 plates of 50000 plaques and then taking plaque lifts onto Hybond N filters.

*Transformation of Arabidopsis*

The cosmids containing DNA from the vicinity of *FCA* were mobilised into *Agrobacterium tumefaciens* C58C1, and the T-DNA introduced into *Arabidopsis* plants as described by Valvekens et al, 1988. Roots of plants grown in vitro were isolated and grown on callus-inducing medium (Valvekens et al, 1988) for 2 days. The roots were then cut into short segments and co-cultivated with *Agrobacterium tumefaciens* carrying the plasmid of interest. The root explants were dried on blotting paper and placed onto callus-inducing medium for 2-3 days. The *Agrobacterium* were washed off, the roots dried and placed onto shoot inducing medium (Valvekens et al, 1988) containing vancomycin to kill the *Agrobacterium* and kanamycin to select for transformed plant cells. After approximately 6 weeks green calli on the roots start to produce shoots. These are removed and placed in petri dishes or magenta pots containing germination medium (Valvekens et al, 1988). These plants produce seeds in the magenta pots. These are then sown on germination medium containing kanamycin to identify transformed seedlings containing the transgene (Valvekens et al, 1988).

25 *EXAMPLE 3 - PLANTS HOMOZYGOUS FOR THE T-DNA INSERTION CARRYING FCA FLOWER EARLIER THAN HETEROZYGOTES.*

Two transformants of each of the four cosmid clones that complemented the *fca* mutant phenotype were selfed

and seed of late and early flowering individuals were collected and plated on kanamycin-containing medium. All the late flowering progeny were kanamycin sensitive whilst progeny from the early flowering individuals were either homozygous or heterozygous for kanamycin resistance. This demonstrates that the kanamycin marker on the T-DNA carrying the region containing the *FCA* gene completely co-segregated with the early flowering phenotype. Thus, complementation to early flowering was due to sequences within the insert of the cosmid. LN was counted for the early flowering individuals either homozygous or heterozygous for the T-DNA insert.

TABLE 1

<u>15</u>	<u>cosmid</u>	<u>K/K</u>	<u>K/-</u>
	CL58I16	10.3 (9)	13 (4)
		9.7 (4)	10.4 (10)
	CL44B23	9.5 (2)	11.8 (6)
<u>20</u>		12 (2)	11.1 (6)
	cAtA1	14.2 (5)	15 (3)
		9.6 (3)	10.8 (5)
	cAtA2	9.1 (7)	9.3 (3)

52

12.5 (3)

14.4 (7)

Analysis of flowering time (as measured by total LN) in transformants showing complementation of the *fca* mutant phenotype. For each cosmid two independent transformants were analysed. The leaf number was counted on F2 individuals (the number of which is shown in the bracket) which were then selfed and progeny sown on kanamycin-containing medium to establish whether the plant was homozygous (K/K) or heterozygous (K/-) for the T-DNA insert.

The results, shown in Table 1 above, indicate that the homozygotes flowered significantly earlier than the heterozygotes in all 8 transformants analysed. Thus increasing the *FCA* gene dosage and therefore most likely the amount of gene product causes earlier flowering.

#### EXAMPLE 4 - ANTISENSE EXPERIMENTS.

A 1184bp BamHI (bp3547, Fig 3)/HindIII (bp4731 Fig 3) restriction fragment from the *FCA* cDNA clone was subcloned into the BamHI/HindIII restriction sites of pBluescriptKSII. The insert was released with the enzymes BamHI and XhoI and subcloned into an *Agrobacterium* binary vector pSLJ6562 (J.Jones, Sainsbury Laboratory). The resulting plasmid contains the CaMV 35S promoter transcribing the *FCA* cDNA fragment to produce antisense RNA, terminated with 3' sequences from the nopaline synthase gene. This plasmid also carries LB and RB *Agrobacterium* sequences for delivery into plant cells and

and a nos5'-kan-ocs3' fusion to allow kanamycin selection for transformants. The construct was introduced into *Arabidopsis thaliana* ecotype Landsberg erecta using the root explant transformation procedure of Valvekens et al  
5 (1988).

Selfed seed from five transformants were collected, sown on kanamycin-containing medium and and 10 kanamycin resistant individuals transplanted to soil. Three of the transformants segregated for a single T-DNA insertion,  
10 the other had two or more. Flowering time, assayed as rosette leaf number was measured. Progeny from four of the five transformants were late flowering, producing 12 rosette leaves, compared to 4 for the fifth transformant. Grown alongside, in these particular conditions, non-  
15 transformed Landsberg erecta and fca-1 plants flowered with ~4 and 11 rosette leaves respectively. Thus the antisense construct (as a single locus) effectively reproduced the late flowering phenotype of the fca-1 mutation.

20

EXAMPLE 5 - CONSTRUCTION OF PROMOTER FUSIONS TO THE FCA  
OPEN READING FRAME.

A genomic SalI-XhoI fragment carrying the whole FCA gene plus 64 bp upstream of the putative start of  
25 translation and 500 bp downstream of the site of polyadenylation was cloned into the XhoI site of the Agrobacterium binary vector pSLJ 6562 (described above). This resulted in a vector carrying a nos-kan fusion for

transformant selection and a fusion where the 35S promoter is driving the *FCA* genomic region (21 exons, 20 introns). Transformants have been made using this construct.

- 5           This construct when introduced into *fca-4* plants corrected the late flowering phenotype causing the plants to flower with 6.4 leaves under a long-day photoperiod. This was similar to wild-type Landsberg erecta which flowered with 6.2 leaves when grown alongside.

10

*EXAMPLE 6 - CONSTRUCTION OF AN FCA GENE LACKING INTRONS - TRANSCRIPTS  $\gamma_A$  AND  $\gamma_B$ .*

The  $\gamma_A$  construct was created by cloning together seven fragments:

- 15           i. an EcoRI (a site present to the insert junction in the multiple cloning site of the vector) - Sall fragment from the cosmid CL43B23. This fragment contains the 5' promoter and untranslated region of *FCA* and the 5' region of the ORF.
- 20           ii. a 425 bp Sall-HindIII restriction fragment from cDNA clone 77B.
- iii. the region of the spliced transcript covering the 5' splice site of intron 3 was generated using RT-PCR with primers cDNAII-BamHI and IanRT1. The product was
- 25           reamplified using cDNAII-1 and RevEx4, digested with Sall and BglII and cloned into pBluescriptKSII digested with Sall and BamHI. A 270 bp HindIII fragment from this



plasmid was then used in the reconstruction of the fully spliced transcript.

iv. a region of the spliced transcript was amplified using RT-PCR and primers BamX and IanRT1. This was  
5 digested with HindIII and BglII and the 52 bp fragment used in the reconstruction of the fully spliced transcript.

v. a region of the spliced transcript was amplified using RT-PCR and primers BamX and Rev404 (position  
10 indicated on Fig.3). A 256 bp ClaI - BamHI fragment was released and gel-purified for use in the reconstruction of the fully spliced transcript.

vi. a ClaI-SpeI fragment was excised from the FCA cDNA clone (the 1811 bp clone isolated from the PRL-2  
15 library)

vii. a SpeI-XhoI fragment, carrying the last ~140bp of 3' untranslated region plus ~500 bp of 3' genomic sequence, was isolated from the FCA genomic clone.

The seven fragments used to construct the FCA gene  
20 lacking introns were assembled in two parts, 5' region and then 3' region, which were then combined.

A. 5' region. Fragment iv was cloned into pBluescriptKSII as a HindIII/ClaI insert. Fragment ii was then cloned into this as an EcoRI/HindIII fragment (the  
25 EcoRI site coming from the multi-cloning site in the cDNA cloning vector). Fragment iii was then cloned into the HindIII site between fragments ii and iv, the correct orientation being determined using an asymmetrically

positioned RsaI site. Fragment i was then cloned into the EcoRI/SalI sites.

B. 3' region. Fragment vii was cloned into the SpeI/XhoI sites present in fragment vi (the XhoI-site  
5 coming from the multiple cloning site in the vector). Fragment v was then cloned into the BamHI site, the correct orientation being determined using an asymmetrically positioned ClaI site.

The 3' region containing fragments v, vi and vii was  
10 then cloned into the plasmid containing the 5' fragments as a ClaI/XhoI fragment.

The  $\gamma_B$  construct was generated by replacing the EcoNI fragment (1503 bp to 2521 bp of spliced transcript) with an EcoNI fragment from a clone derived from RT-PCR from  
15 Ler RNA that contained the alternatively spliced form encoding the full length protein.

The resulting constructs were released from the vector using EcoRI and XhoI and cloned into the EcoRI/XhoI sites of the Agrobacterium binary vector  
20 pSLJ1714 (Jones et al 1992). Transformants carrying this construct have been generated.

Construct  $\gamma_A$  when introduced into Landsberg erecta caused it to flower with 5.6 leaves under a long-day photoperiod. This was slightly earlier than wild-type  
25 Landsberg erecta which flowered with 6.2 leaves when grown alongside. When grown under short-day photoperiod 1/4 of the progeny from the transformant flowered early (with an average of 8.7 leaves). This is significantly

earlier than wild-type Landsberg erecta which flowers with 23.5 leaves under these conditions.

#### EXAMPLE 7 - EXPRESSION IN E.COLI.

5       The  $\gamma_B$  construct, described in Example 6, was digested with Sall and KpnI and cloned into the XhoI-KpnI sites of the *E. coli* expression vector pRSETC (Invitrogen Corp.). The resulting vector has the FCA cDNA cloned in frame with a polyhistidine metal binding domain, which  
10 enables the recombinant protein to be purified away from native *E.coli* proteins using a metal affinity resin (ProBond <sup>TM</sup> Ni<sup>2+</sup>, Invitrogen Corp.). The FCA protein did not bind well to the affinity columns and so was separated from the *E.coli* proteins by excision from an  
15 SDS-polyacrylamide gel. Protein was extracted from the gel slice and used to inject rabbits. A booster jab was given and then two bleeds taken. The antibodies produced detect the FCA protein dot blotted onto nylon membrane at >1/10,000 dilution.

20

#### EXAMPLE 8 - PRIMERS DESIGNED TO AMPLIFY GENES CONTAINING RRM DOMAINS WITH HIGH HOMOLOGY TO FCA.

Based on the homology between *etr-1*, an EST derived from a human brain mRNA (dbest H1995); the *Drosophila*  
25 *sexlethal* protein; the human nervous system proteins HuD, HuC, Hel-N1, and Hel-N2; and the *Xenopus* proteins *elrA*, *elrB*, *elrC*, *elrD* a set of degenerate PCR primers were designed containing two regions of very high homology.

58

Amino acid		F	V	G	S	L	N	K		
OLIGO 1	5'	TTT	GTG	GGG	AGG	CTG	AAC	AAG	C	3'
		C	A	A	TCA	T A	T	A		
		T	T	T	T					
5		C	C	C	C					

Amino acid		R	G	C	F	V	K	Y		
OLIGO 1	3'	TCC	GAC	GCC	GAA	GCA	GTT	TAT	5'	
			A	A	A	A	A	C		
10			T		T		T			
			C		C		C			

EXAMPLE 9 - CONSTRUCTION OF FCA DERIVATIVES TO GENERATE  
 DOMINANT NEGATIVE MUTATIONS AND TO ANALYSE THE EXPRESSION  
 AND SPLICING PATTERN OF THE FCA GENE.

A construct expressing the second open reading frame  
 of transcript  $\alpha_B$  under the control of the FCA promoter,  
 was constructed by deleting the first open reading frame  
 (from 450 bp to 1206 bp). This was done using oligo  
 mutagenesis to introduce a SphI site at the two  
 positions, digesting and religating the vector.

To examine FCA expression FCA promoter-GUS fusion  
 constructs have been made. FCA promoter + exons 1-4 of  
 FCA fused to the  $\beta$ -glucuronidase (GUS) gene have been  
 constructed to monitor the splicing within intron 3. The  
 entire FCA spliced cDNA ( $\gamma_B$ ) with GUS fused in frame at  
 the C-terminus has been made to monitor FCA protein  
 localization within the cell.

*EXAMPLE 10 - IDENTIFICATION OF FCA HOMOLOGUES WITHIN THE ARABIDOPSIS GENOME.*

A four genome equivalent *Landsberg erecta* cosmid  
5 library was screened using low stringency conditions  
(40°C overnight, 1% SDS, 5 x SSC, 0.5% milk powder ) with  
the complete FCA genomic clone. The filters were washed 2  
x 20 min at 45°C in 2 x SSC, 0.5% SDS. After exposure they  
were then rewashed 2 x 20 min, 50°C in 2 x SSC, 0.5% SDS.  
10 61 cosmid clones were picked, plus two negative control  
cosmids. Five of these were additional FCA clones,  
leaving 56 putative FCA homologues. Minipreps were  
prepared from 10 ml o/n cultures of cosmids, digested  
with EcoRI, run on 0.8% gels with positive and negative  
15 controls on each gel and Southern blotted. The blots were  
hybridised separately to 77B and FCA cDNA (originally  
called 61A) (Fig. 7) using the conditions described above  
and then washed at 45°C only.

Of the putative homologues:-

- 20 (a) - 2 cosmids hybridized only to 77B  
(b) - 11 cosmids hybridized only to 61A  
(c) - 31 cosmids hybridized to both cDNAs  
(d) - 13 cosmids difficult to score or showed no  
detectable hybridized

25

- (a) 2 cosmids appear not to be related  
(b) - 49 C 22 and 67 I 3 share common EcoRI  
fragments

60

- 18 G 16 and 7 L 2 " " "

(c) - 39 G 10, 46 H 15, 56 F 2 and 59 A 8 share

common EcoRI fragments,

- 39 G 10 and 56 F 2 share additional frag

5

- 4 H 4 and 45 K 24 share two frags

- at least nine other pairs of cosmids may have

at least one EcoRI fragment in common.

Table 2

Primers	Sequence	bp start Figure 3
cDNAII-BamHI	5' CAGGATCCTTCATCATCTTCGATACTCG 3'	25
cDNAII-1	5' GTCCCTCAGATTCACGCTTC 3'	228
cDNAII-3'a	5' CACTTTTCAAACACATC 3'	1167
cDNAII-3'b	5' GTTCTCTGTACATTAATC 3'	1213
BamX	5' ATTGAGATTCTTACATACTG 3'	2568
RevEx1A	5' TAAGACATGTCTGACAG 3'	2838
RevEx1B	5' GTGATCTGATTGTGCAG 3'	3030
RevEx4	5' TAGACATCTTCCACATG 3'	3145
IanRT1	5' CAATGGCTGATTGCAACCTCTC	3320
IanRT2	5' TCTTTGGCTCAGCAAACCG 3'	3348
Rev404	5' CAATGTGGCAGAAGATG 3'	3673
fca-3'a	5' AGGCCATTGTTTGGCAGCTC	4941
fca-3'b	5' CCCAGCTAAGTTACTACTAG 3'	5003

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CLAIMS:

1. A nucleic acid isolate comprising a nucleotide sequence coding for a polypeptide comprising the amino acid sequence shown in Figure 2.
- 5 2. Nucleic acid according to claim 1 wherein the coding sequence comprises a sequence shown as an exon in Figure 1.
- 10 3. Nucleic acid according to claim 2 wherein the coding sequence comprises the sequences shown as exons in Figure 1.
- 15 4. Nucleic acid according to claim 1 wherein the coding sequence is a mutant, allele or variant of the coding sequence of Figure 1.
5. Nucleic acid according to any of claims 1 to 3 comprising an intron.
- 20 6. Nucleic acid according to claim 5 comprising an intron as shown in Figure 1.
- 25 7. Nucleic acid according to claim 6 wherein said intron is intron 3 of Figure 1.
8. A nucleic acid isolate comprising a nucleotide sequence coding for a polypeptide comprising an amino

65

acid sequence mutant, allele or variant of the FCA amino acid sequence of the species *Arabidopsis thaliana* shown in Figure 2, by way of insertion, deletion, addition or substitution of one or more amino acids, or a homologue  
5 from another species, wherein expression of said nucleic acid in a transgenic plant influences a flowering characteristic of said plant.

9. Nucleic acid according to claim 8 wherein said  
10 flowering characteristic is the timing of flowering.

10. Nucleic acid according to claim 9 wherein said mutant, allele or variant has the ability to advance flowering in a plant.

15

11. Nucleic acid according to claim 9 wherein said mutant, allele or variant has the ability to delay flowering in a plant.

20 12. Nucleic acid according to any of claims 8 to 11 comprising an intron.

13. Nucleic acid according to claim 12 comprising an intron as shown in Figure 1.

25

14. Nucleic acid according to claim 13 wherein said intron is intron 3 of Figure 1.

15. Nucleic acid according to claim 14 comprising the nucleotide sequence of *FCA*  $\alpha_B$ , i.e. that of Figure 3.

5 16. Nucleic acid according to claim 8 that has the nucleotide sequence of *FCA*  $\alpha_A$ , i.e. intron 3 of Figure 1 and all the exons of Figure 1 except for the exon nucleotides indicated in Figure 1 to be within the alternative intron splicing sites around intron 11.

10 17. Nucleic acid according to claim 8 that has the nucleotide sequence of *FCA*  $\gamma_A$ , i.e. all the exons of Figure 1 except for the exon nucleotides indicated in Figure 1 to be within the alternative intron splicing sites around intron 11.

15 18. Nucleic acid according to claim 8 wherein said species other than *Arabidopsis thaliana* is a *Brassica*.

20 19. Nucleic acid according to claim 18 wherein said homologue comprises the amino acid sequence shown in Figure 8b.

20. Nucleic acid according to claim 19 comprising the coding sequence shown in Figure 8a.

25 21. Nucleic acid according to claim 19 wherein the coding sequence is a mutant, allele or variant of the coding sequence of Figure 8a.

22. A nucleic acid isolate comprising a nucleotide sequence coding for a polypeptide comprising an amino acid sequence mutant, allele or variant of the amino acid sequence encoded by the nucleic acid of claim 19, by way of insertion, deletion, addition or substitution of one or more amino acids, which mutant, allele or variant has at least 80% amino acid identity with the sequence of Figure 8b and ability to influence a flowering characteristic of a plant.

10

23. Nucleic acid according to any of claims 1 to 22 further comprising a regulatory sequence for expression of said polypeptide.

15 24. Nucleic acid according to claim 23 comprising an inducible promoter.

25. A nucleic acid isolate comprising a nucleotide sequence complementary to a coding sequence of any of claims 1 to 22, or a fragment of a said coding sequence suitable for use in anti-sense regulation of expression.

26. Nucleic acid according to claim 25 which is DNA and wherein said nucleotide sequence complementary to a said coding sequence or a fragment thereof is under control of a regulatory sequence for anti-sense transcription.

25

27. Nucleic acid according to claim 26 comprising an inducible promoter.

28. A nucleic acid vector suitable for transformation of  
5 a plant cell and comprising nucleic acid according to any preceding claim.

29. A host cell containing heterologous nucleic acid according to any preceding claim.

10

30. A host cell according to claim 29 which is bacterial.

31. A host cell according to claim 29 which is a plant  
15 cell.

32. A plant cell according to claim 31 having said heterologous nucleic acid within its genome.

20 33. A plant cell according to claim 32 having more than one said nucleotide sequence per haploid genome.

34. A plant comprising a plant cell according to any of claims 31 to 33.

25

35. Selfed or hybrid progeny or a descendant of a plant according to claim 34, or any part or propagule of such a plant, progeny or descendant, such as seed.

36. A method of influencing a flowering characteristic of a plant, the method comprising causing or allowing expression of the polypeptide encoded by heterologous nucleic acid according to any of claims 1 to 24 within  
5 cells of the plant.

37. A method of influencing a flowering characteristic of a plant, the method comprising causing or allowing transcription from heterologous nucleic acid according  
10 to any of claims 1 to 24 within cells of the plant.

38. A method of influencing a flowering characteristic of a plant, the method comprising causing or allowing anti-sense transcription from nucleic acid according to  
15 any of claims 25 to 27 within cells of the plant.

39. Use of nucleic acid according to any of claims 1 to 24 in the production of a transgenic plant.

20 40. Use of nucleic acid according to any of claims 25 to 27 in the production of a transgenic plant.

1/26

Figure 1

1 gatctaggtg aaattaatct gaagttttaga aatagatttt cttggaactt  
51 cggagaaaaat atgcttcact caactttttt ttggtgctat atgaacaaag  
101 ataatgggtca tatgaatgta aacgtgtttt gggatgatgt tatcttgttc  
151 catagatgcg gttggaagaa ttgcatttgg actgcaaaaa ctgatggcct  
201 ttatcttttg aattcagcga gcggtgaaga tgtattgtca agaaaatggg  
251 aagttggatg gtgaagccat attttttgctt ttgggtaatt ttttagtaca  
301 tgtatcttgt tgttttttggc aaaaaaaaaa ttgaaataat aaaaaacatt  
351 tgtttttaact ttctctctta ttttgtgtat ttttcatcaa tgatagattt  
401 tttgttttag ttctttatct ataggtcatt taattattag attaatctcc  
451 tgagataata agatcataga ttaaataaca atatttgtgtt tgtgatatat  
501 agagattaca ttttacactt atatatagtg gtaagatttc tttttgcttt  
551 caaaccatta aaaacctgtt aaacgattaa cttgactcaa gacaaagcca  
601 ttgattattg actcatgaat ctagtgactc atgatgaagg agacgaacag  
651 taaatattca tttgattatt ttaggtaaaa ggtagttcag acctagtcatt  
701 atatcctcta aattcatata gtgatgcaag tatttttgcatt tacttagaac  
751 tttatattat tgatcaccca acacatgatt taataaacgc catgaaatgc  
801 atgtactata tcaaaatgtt tctgaagcat atagttgaca tgagaatttt  
851 ggattggact taagaatgtg agagttacct gaaatgtcaa tttttttccc  
901 tttgttaacg aaaactcatt ggaacaattg tatccccctt ttggcagtat  
951 ataaatatat tgatggccca agtagctgta ttttccgtta tcagccaaga  
1001 ctcaataaag tctaccgggc caaatctcaa ctgaatcacc ggtccaacca  
1051 ctattaccgt aactagaccg cttttttcttt ttacattcgc gacaaaaaaa  
1101 tcaaaatttc gagcaactaa attgatctca tcttcaatca AATTCATCAT  
1151 CTTCGATACT CGTTCTTCT CTCTTTGGTT TCATACAGAT CCCAAATTTT  
1201 TAGGGCTCCT AGTCCTTTGA TTTCTTCGAC TGAATCGCA ATTCCTTCTT  
1251 ACGTCAAGCT GGACAGACAC CGAAGGGATC GCCATGAGAG TGGCGGCTAC  
1301 GAGGATTCCT ACCATAACCA CCGAGCCCAT CCCAGAGGTC CATCTCGTCC  
1351 CTCAGATTCA CGCTTCGAAG AGGATGATGA TGATTTTCGC CGCCACCGTC  
1401 GTCGTCGTGG AAGCAGCCCT AGCAATTATC GAATTGGAAT TGGGGGCGGA

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Figure 1 Continued

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1451 GGAGGAGGTA ATGGTGGTCG ACGCTGGGAA GATGACACTC CTAAGGATTT  
 1501 TGATGGTCCC GGAGATGGAG GTTCCGGCA GATGAATGGT CCCCCAGATA  
 1551 GAGTAGATTT TAAGCCTATGGGTCCTCACC ATGGTGGAAG TTTTCGGCCT  
 1601 ATGGGGTTTG CCTACGATGA TGGTTTTTCGT CCAATGGGTC CTAACGGTGG  
 1651 TGTGGGAGGA GAAGGGACAC GGTCAATTGT TGGAGCTCGG TATAACTATC  
 1701 CCGCGAAGTA TCCTCCTTCA GAGAGTCCAG ACAGGAGGAG ATTTATCGGT  
 1751 AAAGCAATGG AGTCTGATTA TTCTGTAAGA CCGACTACAC CGCCGGTCCA  
 1801 GCAGCCTCTT TCCGGTCAGA AAAGAGGGTA TCCTATCTCA GACCATGGCA  
 1851 GCTTTACTGG AACTGgtaag catgagttca ctcttctttc ttctatgtat  
 1901 atttattctt gtagtctgtt aaggttcctg agtgtctctt atttttgtgg  
 1951 gaatcaatga ttagagtatt gaaaggtagt atgggtgtta tgttactgta  
 2001 ttgttgaagg tttttcatgg gatcgactct agaggatcct ttcgattttc  
 2051 ccatgtatgt gataatcaaa actatatgcc atcttcatgt gtatecttat  
 2101 ctgggttaatt tgatttgcag ATGTCTCTGA TCGTAGCAGT ACAGTCAAGC  
 2151 TTTTGTGTTGG ATCTGTACCA AGGACAGCTA CAGAAGAAGA Agtgagttaa  
 2201 tcttggaaat cattgttatc tatatactca ttactgagaa cettttctaa  
 2251 attttttctg ttggttttca tattgtagAT CCGTCCCTAT TTCGAACAGC  
 2301 ATGGAAATGT TCTGGAGGTT GCTCTGATCA AGGACAAGAG AACTGGACAG  
 2351 CAGCAAGgta tgtcaatctc cattttatta ggaaatagtc gtgaattata  
 2401 ctttttaaaa tttcaggtct ccctgaaaag gctgatggga agcaaccca  
 2451 gtctcatcat tggcctccaa ttgtttgcaa caattttcgg gcttattgct  
 2501 tatgcttgcc agcgtcttat ctgtgttcga ttctgtcaca gaagaaggct  
 2551 acctgtgcta agaaagggtt tatgtactta tgttgggcaa atagatttcg  
 2601 ctacttgtgt gtattctaga acttttagatg tgtttgaaaa gtgtagaatt  
 2651 tattgagggc gtttttagagt tggagttaat gtacagagaa ctgaattttg  
 2701 ctgttgccct tatagtggga attgggttata agaacatcgc tttttctc  
 2751 <sup>13</sup>tcctattgaa attcattttc ttactcttc ctctagatgg attgaagatg  
 2801 ttgtgtatgg tcttgacagg atgaatgtat ttttttaagt tggtagtttg  
 2851 ataaggacat gaggttcaaa agatggtttc ttgatttgcc actcctgctg  
 2901 gtcaaagatt tggccgtctt tctaatttta tcatgttggga ggtttggcgt

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Figure 1 Continued

2951 cttcattttc tttcatatca atttatgggt gtgctgtcta ttggttaatg  
3001 atggcattcc ttttaccttt ttggatgagt gatgctggaa tgaatgcgtt  
3051 tctccttttc ttttgttgat ggcctgagga actatgatgg ctatatttct  
3101 ttccactctc tttgaatggc ctgaaatgtg tgctttctgt atggtcgtcc  
3151 ctctcaattt cttggatggc ttgtgatgtg atataccatc tctcgtcata  
3201 ggtgaatgaa tgatttgttt agtagttctt atgtatgtat tttgtatggt  
3251 cccacgtctc tattccttgg atggcttgtg atgtgatata ccatctctcg  
3301 tcatagatga atgaatatct ttgttgagtag ctcttatgtc tgtatggtgg  
3351 cccttgcaat gctgatcgat atttatgtgg aagaaatggt tgatgataga  
3401 ttttttttgt atgctccctt ttcgctaata aagcctttgt gcttgcaagg  
3451 tgcaactgtt attttattat tgaatttcct gttctactac tccatttagt  
3501 tctgtctcta ttttgtcagt gtgaagaaat actagacgat gaatgggtgtg  
3551 tttgtacgtg catagttatt tataaattct tgactttcca agaagttatt  
3601 atttctataa ctgctacacc tttgtggatg gcagaacaaa tgcactgat  
3651 tgtggtgaca taaacacttt tgatcgcggt tgaatgtact agattccata  
3701 caactcttcc ttcagccttg tgaaatatta ttatgttagg tggtgcaaac  
3751 atatggaagg aacctgattg ttttagtttc ttagaatagt ttctgatgtt  
3801 aatacagcat gttgacttca ctctcttgcc cttgatcaat cagcatcagg  
3851 caggggccta attatgtatt acatgaagca atcgtattct tttctgaatt  
3901 agattttttt ccaatgagtt atcttgccca taactgtagt tctttatttg  
3951 aagtcttcaa atgcttgatg tatgggtgacg aaaatgtgta tatgttttgg  
4001 ttttgattat ccgctactca tcaattattg agattcttac atactgaatc  
4051 cgttactttg gacctatagt tatgttttat gttgctaatt aacttgta  
4101 tgtttctaga ttttctttca aatggatcct gcttggaaca atgcagccac  
4151 cctttgtctg aaaggccctc ttgtagatat gttatctgca gatactgact  
4201 gtgttcaatt ttttaatat ttgtttttgcc atattctcca tttgaagaca  
4251 ttaatttatt ctctccaaca actttacatc aataatttaag tggaggctgt  
4301 cagacatgtc ttatgatttt cctactgaac ttatgtgctt tgagtagtac  
4351 atcttggtac tagtacaatt tgatggtaga aggaataagt gaacctgaa  
4401 acagatagct taagtatcag tctttaatgc agGCCTGTGT TTTGTAAAT  
4451 ATGCAACTTC GAAAGATGCG GATAGAGCCA TCAGAGCACT GCACAATCAG

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Figure 1 Continued

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4501 ATCACTCTTC CTGGGgtaat taccctgagg ctttctctta tcaagaacag  
4551 gaaactatag gttgtttcac cttttataat tttgttgatt ccagGGAAC  
4601 TGGTCCTGTT CAAGTTCGAT ATGCTGACGG GGAGAGAGAA CGCATAGgta  
4651 atcaacttcc acacagagta tctaattgtg ctgtcattgt ctagtgttca  
4701 tagccaagac catacgctgc ataagttcag attacaaaaa ttaagaaaat  
4751 gtgggaaatg atatgaactt tatggatggt gatccttttc tttccctggt  
4801 ttctttgcct tactatcaag tgatatagtt ctcttcttct gaagGCACCC  
4851 TAGAGTTTAA GCTTTTGTGTT GGTTCACTAA ACAAGCAAGC CACTGAAAAA  
4901 GAAGTTGAGG AGgtatgttt cgtatcttac tttttgaagt tgttacttat  
4951 gtcagattaa cggaacaggg aagagttcta aacttggata ttattgtgtc  
5001 ccctgttacc tgagttgata attttaaatg actctttgat aaattttgtt  
5051 agtcttacca aagggtgagt gtctagaaaa tctgtgtcaa taatgcaagc  
5101 gcttggacat tctacttact gtgtaatctc ttcttccaat tgatccaact  
5151 gtttgactgt cataatagat aaaattaata aatgtgaacg gctaccttcc  
5201 cagttcaact tatgtgtttc aatttctcat gtaatctttt aacaaactgt  
5251 ttatttggtta ttgctttaac agATCTTTT ACAATTGTT CATGTGGAAG  
5301 ATGTCTATCT CATGCGGGAT GAATATAGAC AGAGTCGTGg tatgttttgt  
5351 aatttgtact agattctata aattatttgt tgtgtgatga tgttgagatg  
5401 gtgaaactgt gtttttcaact ttgtagGATG TGGGTTGTGTT AAATATTCAA  
5451 GCAAAGAGAC GGCAATGGCA GCTATCGATG GTCTCAACGG AACTTATACC  
5501 ATGAGAGtaa gctgtgaatc acataagtat ctgagtttct ctcatatca  
5551 ccctttggac ctgttttgtt tactggcctc taccctttcc ccagGGTTGC  
5601 AATCAGCCAT TGATTGTTTCG GTTGCTGAG CCAAAGAGGC CTAAACCTGG  
5651 CGAGTCAAGg taatgccttg ggtactatat tttgattaat cctaatactc  
5701 ttatcaagta aattgtatat accttcattc tttgttctgt ctgagttata  
5751 tttgtggaga atcttttggga catggtggag agttgggaac cctgttccct  
5801 ctccagttat tactggaatg tgaagcattg ctttctagat atccttaagt  
5851 agtttctgtt tccagGGAAA TGGCACCTCC TGTTGGACTT GTTTCAGGGC  
5901 CTCGTTTTCAGCTTCAGGA CCAAGgtaac tgggtgtgaaa ggagatcatg  
5951 attatgctca ttaggtaatt atatatgttg acttaccctg gtctctcat

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Figure 1 Continued

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6001  ctctatttgt tagGCCTACC TCTAACTTTG GTGACTCTAG TGGGGATGTA
6051  AGCCACACAA ATCCTTGGCG TCCAGCTACT TCACGAAACG TAGGCCCACC
6101  TAGTAACACT GGGATCCGTG GTGCCGGTAG TGACTTTCCC CCTAAACCAG
6151  gtcaagcaac attgccttca aatcaggtga gaacaggttg atgatcatgt
6201  atatcatctt aaatctgcac attcatataa gtaagcgcac agagtttgca
6251  tgtattgtgc gagacaaata aaaagaaagt acttcatata ctgcacacat
6301  gggcttatga caggtgaaaa gaagcatgaa gttctgacct ttcaactttt
6351  catataatgc aacaaacacg atgtgtgttg ctcaaagat atggccttaa
6401  tttgcagttt gtcagttact gaggcaattt tttttttgaa taatttctag
6451  ccctgatgtg agctttttta aatgtaacat tctatattgt tagGGTGGCC
6501  CGTTAGGTGG TTATGGTGTT CCTCCCCCTTA ACCCTCTCCC AGTCCCTGGA
6551  GTTTCATCTT CTGCCACATT GCAACAGgta ctttagctat atttttccaa
6601  ttaagcaaat ctgaaaatgt tgtgatgatt aacttggatt ttcaattggt
6651  tctattccat agCAAAATCG GGCAGCTGGC CAGCATATAA CACCATTAAA
6701  AAAACCTCTT CACAGTCCAC AGGGTCTCCC TCTCCCCCTC CGTCCGCAAA
6751  CTAATTTCCC TGGGGCCCAG GCACCCCTGC AGAATCCTTA TGCTTATAGC
6801  AGCCAGTTGC CTACCTCTCA GCTGCCACCA CAGCAAAACA TCAGTCGTGC
6851  AACTGCTCCT CAAACTCCTT TGAACATTAA TCTACGGCCA ACAACTGTGT
6901  CTCTGCAAC TGTTC AATTT. CCCCTCGTT CCCAGCAGCA ACCGCTACAA
6951  AAGATGCAAC ATCCTCCTTC TGAGCTAGCT CAGCTCTTGT CGCAGCAAAC
7001  TCAGAGTCTA CAAGCAACAT TCCAATCGTC TCAGCAAGCA ATTTCTCAGC
7051  TGCAGCAGCA GGTGCAGTCT ATGCAGCAAC CAAACCAAAA TTTACCCTC
7101  TCACAGAATG GCCGAGCTGG TAAACAACAG gtatgaatat agtctctcag
7151  ttgcatctgc ccagacgggt tcttcagctg ctattgtggt gttttaactt
7201  aaaattattt cctgatagac atcccgtttt ttatccttca tgtgttttag
7251  tattctcccc ttttctaattg ttccctctcgg ctgcttcttt atcagTGGGC
7301  TGGATCTGCA ATTCCAAGAG TGGCTAGCAC CACTGGTTCC ACACCAAGTGA
7351  GCTATGTCGA AACAGCTGCA CCTGCAGTAA GTGAGAGCGT AGGTCTCTGC
7401  AAAATGTAACCT GGACCGAGCA TACCTCGCCT GATGGATTTA AATAATTATTA
7451  CAATGGTCTA ACGGGTGAAA GCAAGgtgag aaacgtgggt cctctttaat
7501  atatttcctt gtgagtttca ggagtattcc tccgtggtta ttgtgctatt

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Figure 1 Continued

7551 gataatcctt acacatgtat attttatatt tgaagtcctt cagtacgtgc  
7601 catattatgt atataattca cttttgtagT GGGAAAAACC TGAGGAAATG  
7651 ATAGTGTTTCG AACGAGAGCA ACAGAAACAG CAACAACATC AAGAGAAGCC  
7701 AACTATACAG CAGTCCCAGA CCCAATTACA GCCGTTGCAG CAACAACCAC  
7751 AACAAGTTCA GCAGCAATAT CAGGGCCAGC AATTACAGCA GCCGTTTAT  
7801 TCTTCACTGg ttggtttcgt tttcatgctg gttacattca aatatttttg  
7851 tcacatgggtt tctaatttgc atatttactc ttgttcattt ggagttgcag  
7901 tatccaactc caggggcccag ccataatact caggtgtata tctgtttaat  
7951 ctgtttactt atttttcatt tcaagatttg attccttgata tgctaactt  
8001 gtggtagaag gagattgacc accttaaagt aaaattcagt agccatgggt  
8051 ttgccagcat ttgaaatac agataacaaa tctctaactg gaatgcctat  
8101 tttcctttct aaaatgcagT ATCCATCATT GCCAGTAGGT CAAAATAGCC  
8151 AGgtacatat ctgaatctgt ggacttattt ttcattgaac tgattgattc  
8201 tcagttacaa cattgacttc ctctgatgcy tagtttttgt aacatatcag  
8251 aataacaaaa acttcatctg attcgtatat tctctgggtg aaaatcttt  
8301 tttcttttct ggaaaatgca gTTCCTATG TCAGGAATTG GTCAGAATGC  
8351 TCAGgtatat atctcatttt gtattaaaca tttcccatac cttctgtacc  
8401 tttgaattta atcacagaac ataatgagtt cttggattta atgtcattt  
8451 aaaaagaaac atcagtata tgacttcctt ccttgggtta aaatgggtta  
8501 ggcagagctt attttctatt ctgtttggat tgtctagGAT TATGCTCGGA  
8551 CACATATACC CGTGGGAGCT GCTTCAATGA ATGATATATC AAGAACTCCA  
8601 CAGgtagtta tggtttttat cagtgattca gaacttctct ctgttcataa  
8651 ttcgtccttt ggtattcaga tgttcttttt cgttgaaacc gttttttcc  
8701 ttaattctct ttacaatcat atctcttttt ccagAGCCG TCAATCTCCC  
8751 CAAGAACTCA TG'GGAAAGAA TAAAGCTTGA Ggttcatatc taccctttct  
8801 ctctctctct ttgtattttt tccataccga aacacattcc aatgtatgtg  
8851 gtttcttttag ttgaagttac ctctgtgttg atcgatactc tacttcagGT  
8901 ACATGAGACG AGGAGCTAAA CTA'CTCAGT AGCTAGATAG AAA'TTCTGG  
8951 AACTAATTAG TCAAGGAGAG GAAAAGCAGC AATGGTAGTG TCC'TAGTCT  
9001 CTGATTTTTT TAGTTAACCC CTTCACTTAT AATAGATAGG CGATCGTAGA

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Figure 1 Continued

9051 CCATCTGCAT TCTATCTTTT CTCTAATCAG ATATCTCCTC CTTTTCATT  
9101 TTAAGAGCTG CCAAACAATG GCCTGTTGTA ACATAGCTAG CGCAAGTTAT  
9151 GTCTCATGTT GTGTTACTAG TAGTAACTTA GCTGGGTAAA CCAAACCTTG  
9201 ATCCAGATTA GGAGTCATAT ATAATTATAT AAATAGAATA TGTACATTCA  
9251 TAGATAgctc atcacttata atgagactag atcttagcaa aatccaactc  
9301 taattgtcat tttcagagat ctatcaattt gtagtttctt gatcttcata  
9351 tatgtgttcg ctcttctaata gattacgtaa aatcagagtc ctacgtaggt  
9401 ggacttcttt aatttttata tagataatta gatatcattc aataagtcgg  
9451 gctttttatth ttagttaatc attctacaat tcttcctaata ctgctatta  
9501 ctaccaccgg gtatccctcc cattttaacc atagcgttct taaaatcctc  
9551 aaagaaaacc gactgatctg ttgcgtaggt ctcaacaatc gcccttgtcc  
9601 ctgggtcttg aaccgctaaa gcctgggtctg atggaagcaa tccctcacc  
9651 gagaggaggt ttacatagta ctggttgatc aatgttgatg gagtcaccaa  
9701 gtcaagctga gtgataccta cactgggccc aacagtcgag cataactgtt  
9751 gcagtgactc gag

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Figure 2

1 MNGPPDRVDF KPMGPHHGGS FRPMGFAYDD GFRPMGPNGG VGGEGRSIV  
51 GARYNYPKY PPSESPDRRR FIGKAMESDY SVRPTTPPVQ QPLSGQKRGY  
101 PISDHGSFTG TDVSDRSSTV KLFVGSVPRT ATEEEIRPYF EQHGNVLEVA  
151 LIXDKRTGQQ QGCCFVKYAT SKDADRIRA LHNQITLPGG TGPVQVRYAD  
201 GERERIGTLE FKLFVGS LN KQATEKEVEEI FLQFGHVEDV YLMRDEYRQS  
251 RGC GFVKYSS KETAMAAIDG L NGTYTMRGC NQPLIVRFAE PKRKPGE SR  
301 DMAPPVGLGS GPRFQASGPR PTSNEGDSSG DVSH TNPWRP ATSRNVGPPS  
351 NTGIRGAGSD FSPKPGQATL PSNQGGLGG YGVPPLNPLP VPGVSSSATL  
401 QQENRAAGQH ITPLKKPLHS PQGLPLPLRP ETNFPGGQAP LQNPYAYSSQ  
451 LPTSQ LPPQQ NISRATAPQT PLNINLRPTT VSSATVQFPR RSQQQPLQKM  
501 QHPPSELAQL LSQQTQSLQA TFQSSQQAIS QLQQQVQSMQ QPNQNLPLSQ  
551 NGRAGKQQWA GSAIPRVAST TGSTPVSYVQ TAAPAVSQSV GSVKCTWTEH  
601 TSPDGFKYYY NGLTGESKWE KPEEMIVFER EQQKQQQHQE KPTIQQSQTQ  
651 LQPLQQQPQQ VQQQYQGQQL QQPFYSSLYP TPGASHNTQY PSLPVGQNSQ  
701 FPMMSGIGQNA QDYARTHIPV GAASMNDISR TQQSRQSPQE LMWKNT

Figure 3

1 AAATTGATCT CATCTTCAAT CAAATTCATC ATCTTCGATA CTCGTTTCTT  
51 CTCTCTTTGG TTTCATACAG ATCCCAAATT TCTAGGGGCTC CTAGTCCTTT  
101 GATTTCTTCG ACTGGAATCG CAATTCCCCA CTACGTCAAG CTGGACAGAC  
151 ACCGAAGGGA TCGCCATGAG AGTGGCGGCT ACGAGGATTC CTACCATAAC  
201 CACCGAGCCC ATCCCAGAGG TCCATCTCGT CCCTCAGATT CACGCTTCGA  
251 AGAGGATGAT GATGATTTTC GCCGCCACCG TCGTCGTCGT GGAAGCAGCC  
301 CTAGCAATTA TCGAATTGGA ATTGGGGGGCG GAGGAGGAGG TAATGGTGGT  
351 CGACGCTGGG AAGATGACAC TCCTAAGGAT TTTGATGGTC CCGGAGATGG  
401 AGGTTTCCGG CAGATGAATG GTCCCCCAGA TAGAGTAGAT TTTAAGCCTA  
451 TGGGTCTCA CCATGGTGGA AGTTTTCGGC CTATGGGGTT TGCCTACGAT  
501 GATGGTTTTTC GTCCAATGGG TCCTAACGGT GGTGTGGGAG GAGAAGGGAC  
551 ACGGTCAATT GTTGGAGCTC GGTATAACTA TCCCGCGAAG TATCCTCCTT  
601 CAGAGAGTCC AGACAGGAGG AGATTTATCG GTAAAGCAAT GGAGTCTGAT  
651 TATTCTGTAA GACCGACTAC ACCGCCGGTC CAGCAGCCTC TTTCCGGTCA  
701 GAAAAGAGGG TATCCTATCT CAGACCATGG CAGCTTTACT GGAAGTATG  
751 TCTCTGATCG TAGCAGTACA GTCAAGCTTT TTGTTGGATC TGTACCAAGG  
801 ACAGCTACAG AAGAAGAAAT CCGTCCCTAT TTCGAACAGC ATGGAAATGT  
851 TCTGGAGGTT GCTCTGATCA AGGACAAGAG AACTGGACAG CAGCAAGGTA  
901 TGTCAATCTC CATTTTATTA GGAAATAGTC GTGAATTATA CTTTTTAAAA  
951 TTTCAGGTCT CCCTGAAAAG GCTGATGGGA AGCAACCCCA GTCTCATCAT  
1001 TGGCCTCCAA TTGTTTGCAA CAATTTTCGG GCTTATTGCT TATGCTTGCC  
1051 AGCGTCTTAT CTGTGTTTGA TTCTGTCACA GAAGAAGGCT ACCTGTGCTA  
1101 AGAAAGGGTT TATGTACTTA TGTTGGGCAA ATAGATTTCG CTAATTGTGT  
1151 GTATTCTAGA ACTTTAGATG TGTTTGAAAA GTGTAGAATT TATTGAGGGT  
1201 GTTTTAGAGT TGGAGTTAAT GTACAGAGAA CTGAATTTTG CTGTTGCCTT  
1251 TATAGTGGGA ATTGGTTATA AGAACATCGC TATTTTCCTC TCCCTATTGA  
1301 AATTCATTTT CTTTACTCTT CCTCTAGATG GATTGAAGAT GTTGTGTATG

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Figure 3 Continued

1351 GTCTTGACAG GATGAATGTA TTTTTTTAAG TTGGTAGTTT GATAAGGACA  
1401 TGAGGTTCAA AAGATGGTTT CTTGATTTGC CACTCCTGCT GGTCAAAGAT  
1451 TTGGCCGTCT TTCTAATTTT ATCATGTTGG AGGTTTGGCG TCTTCATTTT  
1501 CTTTCATATC AATTTATGGG TGTGCTGTCT ATTGGTTAAT GATGGCATTG  
1551 CTTTTACCTT TTTGGATGAG TGATGCTGGA ATGAATGCGT TTCTCCTTTT  
1601 CTTTTGTTGA TGGCCTGAGG AACTATGATG GCTATATTTT TTECACTCT  
1651 CTTTGAATGG CCTGAAATGT GTGCTTTCTG TATGGTCGTC CCTCTCAATT  
1701 TCTTGGATGG CTTGTGATGT GATATACCAT CTCTCGTCAT AGGTGAATGA  
1751 ATGATTTGTT TAGTAGTTCT TATGTATGTA TTTTGTATGT TCCCACGTCT  
1801 CTATTCCTTG GATGGCTTGT GATGTGATAT ACCATCTCTC GTCATAGATG  
1851 AATGAATATT TTGTTGAGTA GCTCTTATGT CTGTATGGTG GCCCTTGCAG  
1901 TGCTGATCGA TATTTATGTG GAAGAAATGT TTGATGATAG ATTTTTTTTG  
1951 TATGCTCCCT TTTGCTAAT CAAGCCTTTG TGCTTGCAAG GTGCAACTGT  
2001 TATTTTATTA TTGAATTTCC TGTCTACTA CTCCATTTAG TTCTGTCTCT  
2051 ATTTTGTGAG TGTGAAGAAA TACTAGACGA TGAATGGTGT GTTTGTACGT  
2101 GCATAGTTAT TTATAAATTC TTGACTTTCC AAGAAGTTAT TATTTCTATA  
2151 ACTGCTACAC CTTTGTGGAT GGCAGAACAA ATGCATCTGA TTGTGGTGAC  
2201 ATAAACACTT TTGATCGCGG TTGAATGTAC TAGATTCCAT ACAACTCTTT  
2251 CTTCAGCCTT GTGAAATATT ATTATGTTAG GTGGTGCAA CATATGGAAG  
2301 GAACCTGATT GTTTTAGTTT CTTAGAATAG TTTCTGATGT TAATACAGCA  
2351 TGTTGACTTC ACTCTCTTGC CCTTGATCAA TCAGCATCAG GCAGGGGCCT  
2401 AATTATGTAT TACATGAAGC AATCGTATTC TTTTCTGAAT TAGATTTTTT  
2451 TCCAATGAGT TATCTTGCCC ATAAGTGTAG TTCTTTATTT GAAGTCTTCA  
2501 AATGCTTGAT GTATGGTGAC GAAATGTGT ATATGTTTTG GTTTTGATTA  
2551 TCCGCTACTC ATCAATTATT GAGATTCTTA CATACTGAAT CCGTTACTTT  
2601 GGACCTATAG TTATGTTTTA TGTTGCTAAT TAACTTGTAC ATGTTTCTAG  
2651 ATTTTCTTTC AATGGATCC TGCTTGGACA AATGCAGCCA CCCTTTGTCT  
2701 GAAAGGCCCT CTTGTAGATA TGTTATCTGC AGATACTGAC TGTGTTCAAT  
2751 TTTTAAATAT TTGTTTTTGC CATATCTCC ATTTGAAGAC ATTAATTTAT

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Figure 3 Continued

2801 TCTCTCCAAC AACTTTACAT CAATATTTAA GTGGAGGCTG TCAGACATGT  
2851 CTTATGATTT TCCTACTGAA CTTATGTGCT TTGAGTAGTA CATCTTGTTA  
2901 CTAGTACAAT TTGATGGTAG AAGGAAAAGT TGAACCCTGA AACAGATAGC  
2951 TTAAGTATCA GTCTTTAATG CAGGCTGTTG TTTTGTAATA TATGCAACTT  
3001 CGAAAGATGC GGATAGAGCC ATCAGAGCAC TGCACAATCA GATCACTCTT  
3051 CCTGGGGGAA CTGGTCCTGT TCAAGTTCGA TATGCTGACG GGGAGAGAGA  
3101 ACGCATAGGC ACCCTAGAGT TTAAGCTTTT TGTTGGTTCA CTAAACAAGC  
3151 AAGCCACTGA AAAAGAAGTT GAGGAGATCT TTTTACAATT TGGTCATGTG  
3201 GAAGATGTCT ATCTCATGCG GGATGAATAT AGACAGAGTC GTGGATGTGG  
3251 GTTTGTATAA TATTCAAGCA AAGAGACGGC AATGGCAGCT ATCGATGGTC  
3301 TCAACGGAAC TTATACCATG AGAGGTTGCA ATCAGCCATT GATTGTTCCG  
3351 TTTGCTGAGC CAAAGAGGCC TAAACCTGGC GAGTCAAGGG ACATGGCACC  
3401 TCCTGTTGGA CTTGGTTCAG GGCCTCGTTT TCAAGCTTCA GGACCAAGGC  
3451 CTACCTCTAA CTTTGGTGAC TCTAGTGGGG ATGTAAGCCA CACAAATCCT  
3501 TGGCGTCCAG CTACTTCACG AAACGTAGGC CCACCTAGTA ACACTGGGAT  
3551 CCGTGGTGCC GGTAGTGACT TTTCCCCTAA ACCAGGTCAA GCAACATTGC  
3601 CTTCAAATCA GGGTGGCCCG TTAGGTGGTT ATGGTGTTC TCCCCTTAAC  
3651 CCTCTCCCAG TCCCTGGAGT TTCATCTTCT GCCACATTGC AACAGGAAAA  
3701 TCGGGCAGCT GGCCAGCATA TAACACCATT AAAAAAACCT CTTACAGTC  
3751 CACAGGGTCT CCCTCTCCCC CTCCGTCCGG AACTAATTT CCCTGGGGGC  
3801 CAGGCACCCT TGCAGAATCC TTATGCTTAT AGCAGCCAGT TGCCTACCTC  
3851 TCAGCTGCCA CCACAGCAA ACATCAGTCG TGCAACTGCT CCTCAAACCTC  
3901 CTTTGAACAT TAATCTACGG CCAACAACCTG TGTCTTCTGC AACTGTTCAA  
3951 TTTCCCCCTC GTTCCCAGCA GCAACCGCTA CAAAAGATGC AACATCCTCC  
4001 TTCTGAGCTA GCTCAGCTCT TGTGCGAGCA AACTCAGAGT CTACAAGCAA  
4051 CATTCCAATC GTCTCAGCAA GCAATTTCTC AGCTGCAGCA GCAGGTGCAG  
4101 TCTATGCAGC AACCAAAACCA AAATTTTACCA CTCTCACAGA ATGGCCGAGC  
4151 TGGTAAACAA CAGTGGGCTG GATCTGCAAT TCCAAGAGTG GCTAGCACCA

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Figure 3 Continued

4201 CTGGTTCGAC ACCAGTGAGC TATGTGCAAA CAGCTGCACC TGCAGTAAGT  
4251 CAGAGCGTAG GTTCTGTCAA ATGTACCTGG ACCGAGCATA CCTCGCCTGA  
4301 TGGATTTAAA TATTATTACA ATGGTCTAAC GGGTGAAAGC AAGTGGGAAA  
4351 AACCTGAGGA AATGATAGTG TTCGAACGAG AGCAACAGAA ACAGCAACAA  
4401 CATCAAGAGA AGCCAACTAT ACAGCAGTCC CAGACCCAAT TACAGCCGTT  
4451 GCAGCAACAA CCACAACAAG TTCAGCAGCA ATATCAGGGC CAGCAATTAC  
4501 AGCAGCCGTT TTATTCTTCA CTGTATCCAA CTCCAGGGGC CAGCCATAAT  
4551 ACTCAGTATC CATCATTGCC AGTTGGTCAA AATAGCCAGT TTCCTATGTC  
4601 AGGAATTGGT CAGAATGCTC AGGATTATGC TCGGACACAT ATACCCGTGG  
4651 GAGCTGCTTC AATGAATGAT ATATCAAGAA CTCAACAGAG CCGTCAATCT  
4701 CCCCAGAAGC TCATGTGGAA GAATAAACT TGAGGTACAT GAGACGAGGA  
4751 GCTAAACTAT CTCAGTAGCT AGATAGAAAT TTCTGGAACT AATTAGTCAA  
4801 GGAGAGGAAA AGCAGCAATG GTAGTGTCCT TAGTCTCTGA TTTTTTTAGT  
4851 TAACCCCTTC AGTTATAATA GATAGGCGAT CGTAGACCAT CTGCATTCTA  
4901 TCTTTTCTCT AATCAGATAT CTCCTCCTTT TTCATTTTAA GAGCTGCCAA  
4951 ACAATGGCCT GTTGTAACAT AACTAGCGCA AGTTATGTCT CATGTTGTGT  
5001 TACTAGTAGT AACTTAGCTG GGTAACCAA ACTTTGATCC AGATTAGGAG  
5051 TCATATATAA TTATATAAAT AGAATATGTA CATTCATAGA TAAAAA  
5101 AAAAAAAAAA AAA

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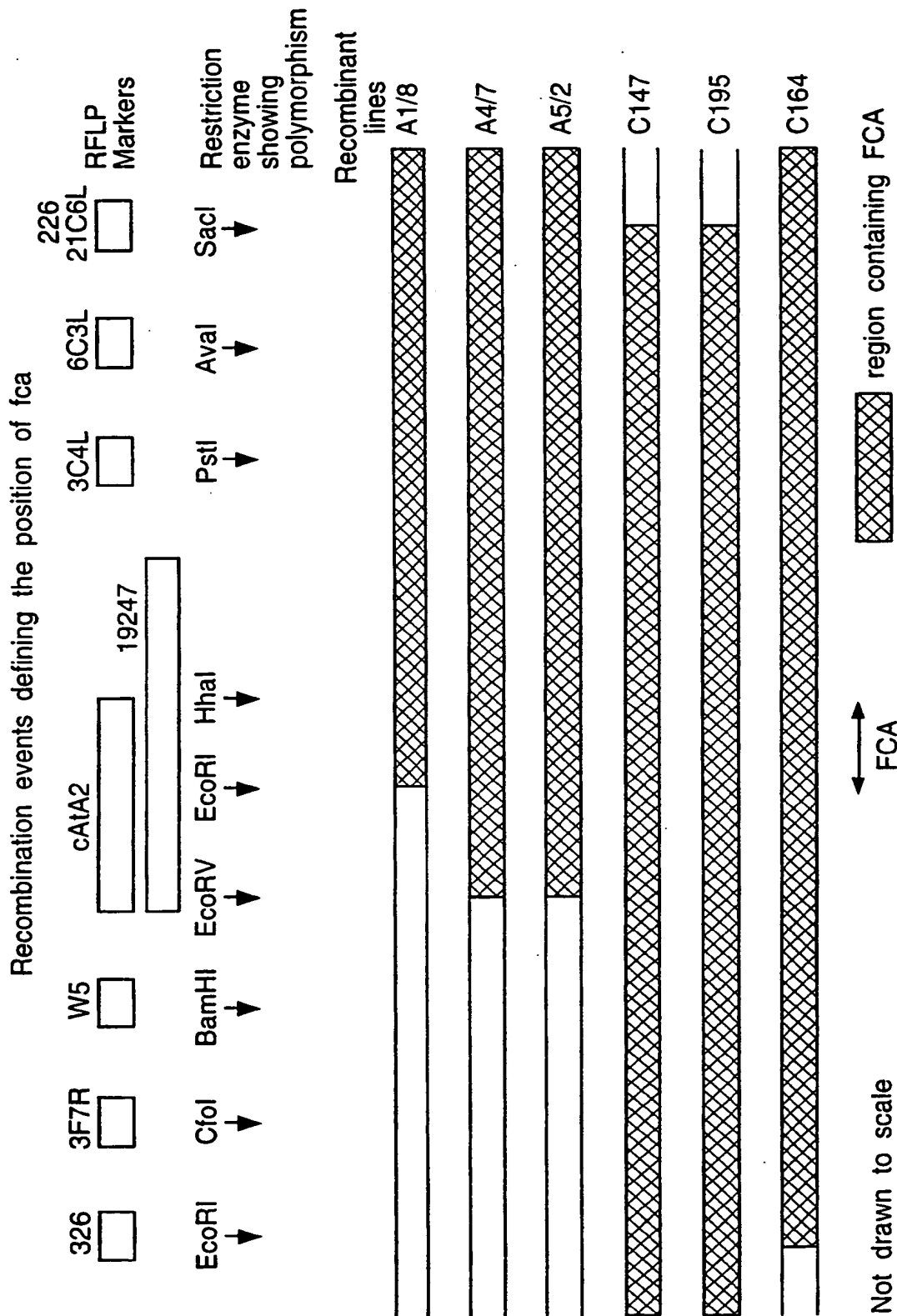
## RNA Binding Domain

## Homology in C-terminal region

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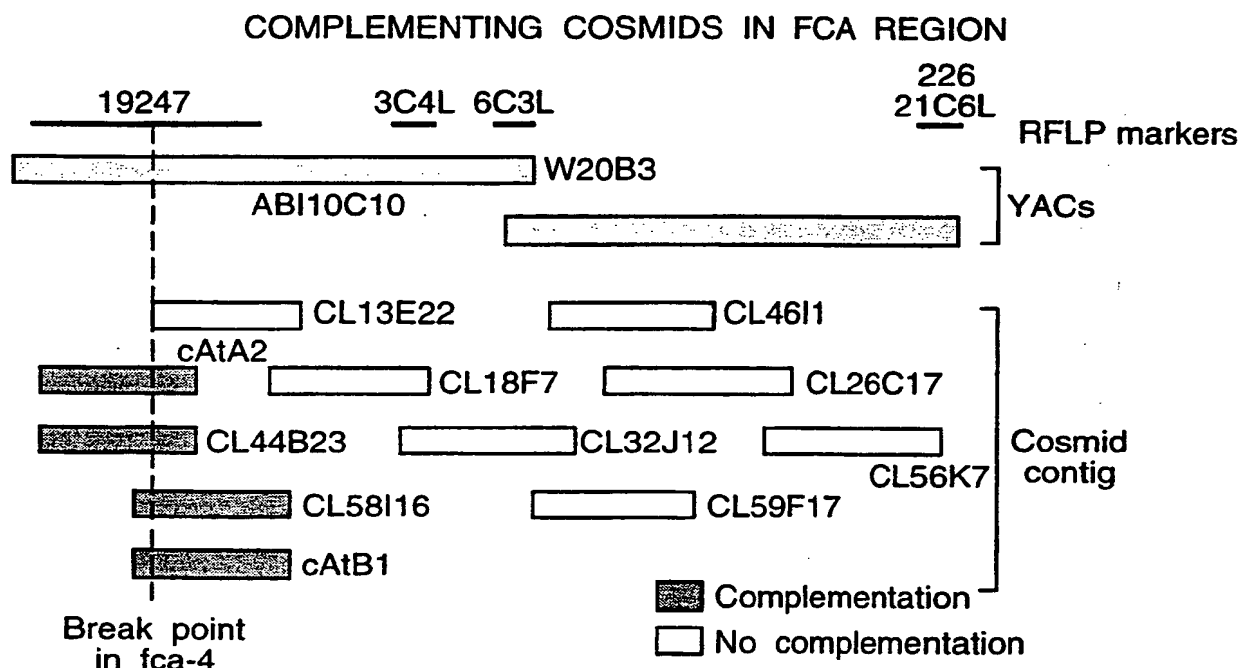
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Fig.5.



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Fig.6.



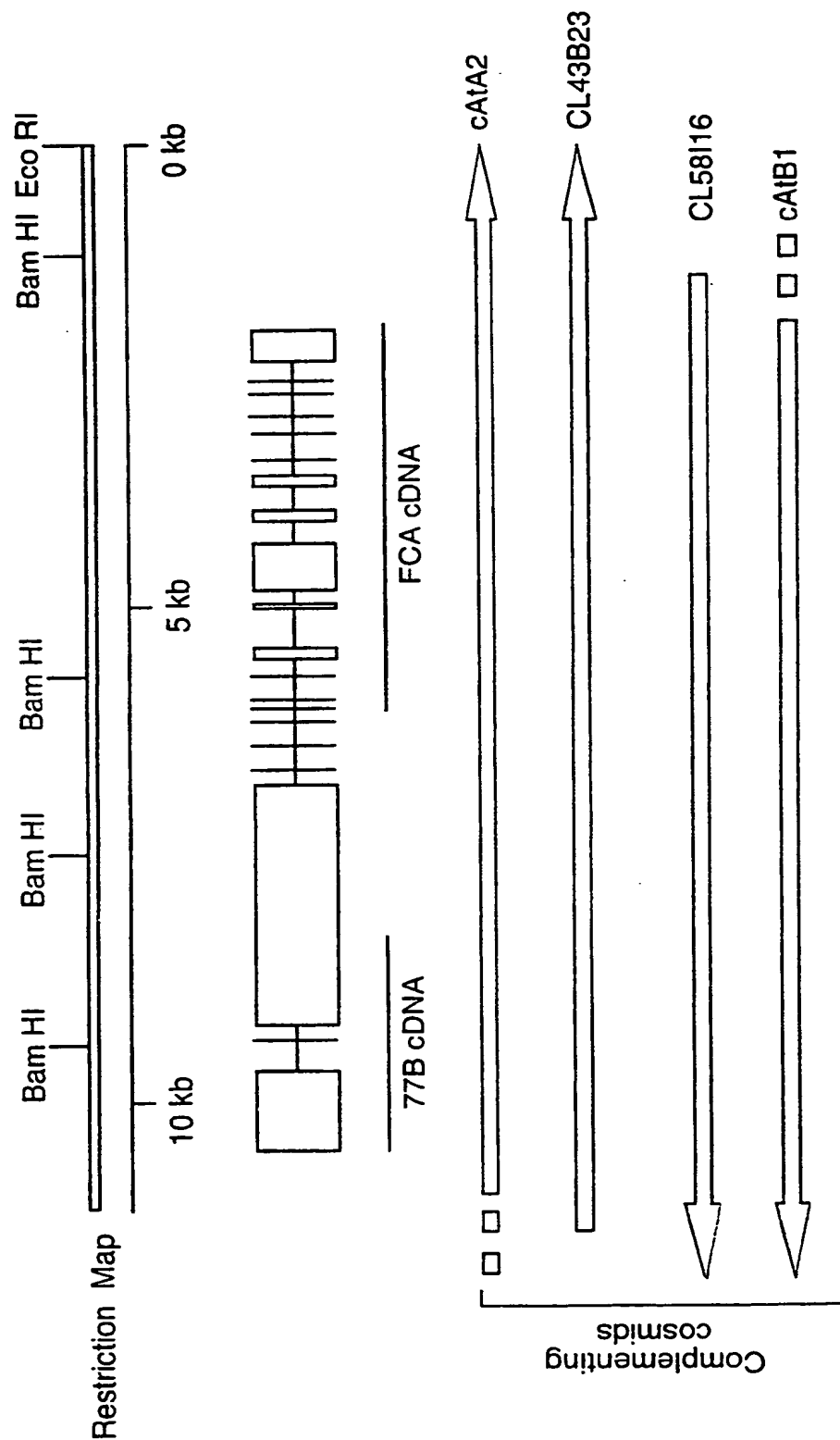
Cosmid No. transformants complementing No. transformants generated

cAtB1	5	5
cAtA2	3	4
CL44B23	7	8
CL58I16	6	11
CL13E22	0	4
CL46I1	0	1
CL32J12	0	4
CL18F7	0	4
CL59F17	0	2
CL26C17	0	2
CL56K7	0	4

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Fig.7.



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Figure 8a

1 GTTAACGGAT CACACAGTAT AATATAAAAC TAGGTGTTTT GCCCGCACAT  
51 GCGAGCATAA TTTTCTCATC AATACTTATT AGTTTATATC TTATTAATCT  
101 AAAACCAGCA TGATAAGTTA TTATTTATGT TTTCAGATAG TTAAATCAAA  
151 CATCAAAGTA TTTATATATG TCAAATATTT TATCAAAAAT ATATACTTAT  
201 TATTGTGTTA AATTTTTTTAA AACACTCATA TCTTAGAAAT AGTTTAGAAA  
251 ATATCTTTAT ATAAATGTTT TTTAACTTTT ATAATAAAAA TATTGTTTTT  
301 AGATAGCAAC AAAATATATA TAGAATTAAC TTATTTTTAA ATTTTTTGAT  
351 AATTTTATTA TATTATTTAA GAATCAATTA TTTATATTAA TATAACATAT  
401 AATTTTCACT GATTAAATAA AATTCGTTTT TAATTATATA AATTCATTAA  
451 GAGTATGTT TTAATAACAC ATTAGCGAAC ATCAGCTAGA AATTAATAAT  
501 AAATCAATAA CCTAGCTAAA AGTCTAAAAC CTAATAAAAT ATGACAAATA  
551 AGAAAAATTA ACTAAATTTT AATATAAAAT ATAAATTTAA TATTACTAAA  
601 ATAAAAATCA TTTTAAATAT ATATAAGATT CTTAAGGGTA TTTTAAAT  
651 TAATAAATTA GTGACTTAGC TAAAAATAAA TAATAAATCA ATGATTTAGC  
701 TAAAACCTAA TAAAACATG ACAAATAAGC AAATTTACTA AAATTATTGA  
751 TAATATAAAA TATGATTGAT TCTTTAATAC AAAATTAAAA TAAGAGTTTT  
801 TTTAAATCAA ACATAAGTCT GCCGTATCGG TGTAAAAAAA AAAATCATT  
851 ATAGTGTCGT AGGAATTATG TATTTCCATT AGCGAATAAA ATTGAAGCAG  
901 AGTGTTGGAG GATAGCTCAA CGTATAGGCG AGATTATGGA GATTGATATG  
951 GGAGTTGCCG TAACGGACAC AACTGTTTCT CTGCAAAGAA ACGCTCCTAC  
1001 TAGATGGACA TGTCAAGTTG ATGCATCCTG GATAAATGAA AGAAACATAT  
1051 CTGGACTTGG CTTTG'IGTTA ATGGATGGTG ACTTCCCAAT ACTGTTTGTA  
1101 TCAACGGCCG ATATACACGC ACCAAATCAC CACTGCAAGC GGAACGTGAA  
1151 GGTTTGCTAT GGGCAATGCA AGAGATACTG AAGTTTGGAC GCAGAGTGAT  
1201 GGTCTTTCAA TCGACTATGA ACAACTGGTT ATACTCATTC AAAAGGAGGA  
1251 AGATGGCCTG CTGGGACTCG GAGCTCGACG AAATACAAGT TGTATCAAAG  
1301 AATTTTCTGA AATTTCTATT GCTTATATTC CTAGATCTTT AAAATTCCGT  
1351 ACGAATAGCC TAGCAAAAGG TGTCGATCAC CCGCATCACG ATCAGCTTTT

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Figure 8a Continued

1401 GTAACCCTTT GCACCAGTGG CTAGCCCACA GCTAGCATGA GGGTGCAAAA  
1451 GAGAATAAGT CGAAACAAGC TAGCATGAGG GTGCCAAAAA AGAGAATAAA  
1501 GTCGAAAGTA AAACCTGAATA TCCAATGAAC AAAATTATCA GAAATCCATA  
1551 TTTATGTGGA TGTCTATATG GGACAAACAA TTTTTTTAGA TCAATCCTAA  
1601 AATATATAAT TTAACAAAAC CATTTAAACA AACCATCAAA ATTTTGAATA  
1651 TTACACCAAA AAAAAATATA AAGACCAACT ATATTATATT CATGTATAAT  
1701 GTGTAGTGGT AAGATTCAAA AAAATTAACT TACTTTACAG TAAGGGAAAA  
1751 TTAGATTTTT TATTCCATAT TTACAGTAAA AACATAACAT TTTATAAAAC  
1801 TAAACAATTG ACATAATAGT ACAAATATG AAAAAAAAT CAAAATACTA  
1851 AGAACCTACT ATTAGTTAAA TTAAGTACAG TCAAGTCAAC TAGTATGTGA  
1901 ATGAGATTTA ACTTACAAAT TCATTACGAG ACAATAGCAC ATTTAGAAGA  
1951 ATAACATGTA GATTGATGTG CACACAAAAA AAAACCAACG GGTACAAATG  
2001 TTAACCGCTC CACCGGTCGA ACCATAATCC AGACCGGTTT TGCTATTTAA  
2051 ACCGCTCAAA TCGCAAAGTA CGTTTCGCTT ACTTCCAGCA AACCACCATT  
2101 GATCTCTCCT CCAATTCACA AATCCAATTT CTCTAGGGTT TGATTTCCTC  
2151 GACTTGAATT GCATTTCCAT CCGAATTTCC CCAAATTCGT CAAGCTGGAT  
2201 AGGCACCGAG GGGATCGCCA CGAGAGTGCC TTACGACGAT TCCTACCGTA  
2251 ACCACCGAGC TCACCTAGAG GTCCCCCTCT ACTCTCAGAT TCACCTCCA  
2301 TGTCACGTTT CGGCGAGGAT GACGAAGGTT TCAGCCGCCG TCGTCGCCGT  
2351 GGAAACAGCC TAGCAATTAT CAGTTGGATG GGACAGAGGA GGTGGCGATC  
2401 GACGCTGGGA AGATGACGGC CACGATCGTA TTTCACAGAG AGGCGTGGGA  
2451 GAGTAGAATT TCAGCCTATG GGTTATGGCT TCGACGGAGG TTTCCGCCG  
2501 ATGAGTCGCG ACGGAGGATT TTGGCCTAAC GTGCCAGTGA ATTTCCGCC  
2551 ATCGGAAAGT CCAGATGCAG GGGGATATTC CGGCGGCAGG GGATTTCAAT  
2601 CAACGGGGCC TGTCTACTCT GTGAGATTGA CTTACCGCC GATCCAGCAG  
2651 CCTCTTCTTG GTACAGAAAAG AGGTCTGTCCT CTCTCGGAGC AGAGTAGCTT  
2701 TACTGGAAC TGTAAAGCTTG GGTCACTCT ACTGTAATCG AGTTGTTTAG  
2751 AGTTAACAGT GTTTCATTTT ATACTTGAT GTGATAATCA GGCTATTTC  
2801 AAACATAATT ACCTTTACTG GATCATTCGT TTTGCAGATT TACTGATAGT

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Figure 8a Continued

2851 AGCAGTATGG TGAAGCTTTT TGTGGCTCT GTACCAAGGA CAGCTACAGA  
2901 AGAAGAAGTG AGTTCATCTT TTTCTTATTT TCCTAATTTT TTCTCAATAT  
2951 ATATGCACTT TCTTGAGGCA ATCTAAACCA CGAAGCTCGT AGACTCTGTT  
3001 CATAAGCCGT TCTTGTTTAT CATTTTGGTT TTCATAGGTC CGTCCCTTTT  
3051 CGAACAACAC GGTAATGTG CTTGAGGTTG CTTTTATCAA GGACAAGAGA  
3101 ACAGGACAGC AGCAAGGTAT GTTTATCTCC ATTTTACTAG GAACAGTCGT  
3151 GATTTATGCT TCTAAATTTT TCAGGTCTCC TGAAAAGGCT GATGGGAACG  
3201 AACCCAGTC TCATCATGG CCTCCATTAG TTTTCAACAA TTTTCGGGCT  
3251 TTGCTTATG CTAGCGAGCG TCTTATCTGT GTTGCTTTGG CACAGAAGAA  
3301 GGCTGCCTGT TTAGTTTACT AAGAAAGGGT TTTTGTATTG ACCTTGGTAA  
3351 AATAGTTTTT GCGACTTGTG TCCATCCTAG AACCTTAGTT GTGTTTGAAC  
3401 AGTGTAGCAG ACTTTATCAT GTTTTAGAGT TGGAGTTAAT GTACATAAAA  
3451 TTGAACAGAT GTTTTACTGT TGCCTTTTAG TTGGCACTGG TTTAAAGAAC  
3501 GTTGTTTTCT CCTTTCCTAT TGAATTCAGT ATCTCTTTAC TCTTCCTTTC  
3551 GATGAATGAA AATGGTGTAT ATGGTCTTGA CTGGATGAAT GTATTTTTAC  
3601 TTGGTAGTCT TACAACGTTT ATAAAATGGT TTGATTGATA AACCACCCCT  
3651 GCTAGTCAAT ATTTGGCAGT TTCTTAGTGA TTATATCATG TTGGATGTTT  
3701 TGTTTCTTTA GTTCTTTTAA TATCAACTTT GGATGTACCG TCTCTATTGG  
3751 TTGATGATGA AATTATTTTT TACCATTTTG GATGCTTGAT GCCTTAATGA  
3801 ATGGATCTTT CCTTTTTTTC TTATTGTGGA TGGCCGAGGA ACTATAATGA  
3851 ATGTCTCTT CGCTTTTTTT GAATGGCCTG GGATGTGGAC TTCTTGATG  
3901 TTCTCACTTT CATTGATGAA TGAAGTTTC GTTGAGTAGC TCTATTGTTC  
3951 TGTATGGTAA CGCTAACACT GCTGATCTAC ATTATGTGGA AGAGATCATA  
  
4001 TGTTCTAATGA TATTTTTTTTT CTATGTACCT TTCACCAACC AAGCTCAAAA  
4051 GCTTGGTTTC AGTTTTTAGT GGTCTTATTC TATATAGAGC TTGGTTTCAG  
4101 TTTTTAGTGG TCTTATCTA TATATTGAGA TTGCTCTTGA AAAATTCCAT  
4151 CAAAGTCTG TCTTATGAT GCAAGTGTGA AGAATTACTA GATGATGAGT  
4201 GATGTATTAT TTAATAATTC GGGACTTTC AAGAAGTTAT TGTACGGTGA

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Figure 8a Continued

4251 CATAAAAGCT TTTACTCATC CCGTTATCAC GGTTTGACTG TAGTAGATTT  
4301 GACACATTCC TTGGTTTGAA ATGTTACATG GTGCTAAGAT ATGGAAGGCA  
4351 ACGATTATTA TAATTTCTTA GAAATACGTC TTAGCTTTCA CTCGCTCTCA  
4401 TTGCTTCGAT CAGCATCAGG CATGAGCCGC CTTAGTATGT ATTTAATGAA  
4451 GCAAGTGTCA TTCTTCTCTA TATGCAACTA TTACCAATGA ATTGACGTTG  
4501 GGTGTGGTT ATGTCTCTCA GAACTGTAAT TCTTTTTGTG AATGTCGTCA  
4551 AATGTGTGGT GTATGTTGTA TGGTGTATGG TGACGAAAAT GTGATGTATG  
4601 GCTCTAGTTT TAATTATATC ATTTGTTACT TAGCAGTGAT TGAGAACTCT  
4651 TAÄCTTGTA TTTTATCTAA TTTTTTTTTG CAGTGATTGG ATTCTTTTTG  
4701 CGTAATATAT ATTTTATTG CAAATACCGA CTGTGTTCTT TTTAAATAGT  
4751 TTAAAGGCAT ATGCTTTATT TGAAGCACAT TAGTTTATTA TTCTCTCCAT  
4801 CAAATCTACT ACAGTAATGT AAGTCGAGGC TGTCAGGACA TGTCTTATGA  
4851 TTTTCGTACT GAAACTTATG TGCTTTCAAT GTGGTCGTGG CTTGTACATT  
4901 TGTAAGAAA CTATTTACTA GTATCTCTTG ATGTTTGATG GAGGGACAAG  
4951 TGGAACCTTG AACAGAAGCT TATGTAGCAG TCTTTAATGC AGGCTGTTGT  
5001 TTTGTAAAAT ATGCAACTTC TGAAGATGCG GATAGGGCCA TTAGAGCATT  
5051 GCACAATCAG ATCACTCTTC CTGGGGTAAC TACCATTGAT GCCTTCTCTT  
5101 ATCAAGGACA GGAAAATACA GGTAACTCT ATCTTTACAA TTTGCTGATT  
5151 CCCAGGGAAC TGGCCTTGTT CAAGTTCGAT ATGCTGATGG GGAGAGAGAA  
5201 CGCATAGGTA ATCAACTTTC GCGCCATATT ATCTGAATCT GGCCTTCATT  
5251 GTCTGGTATA CATAGGGTGA CCATACGCTG TACAAATTCA AATTACGAGA  
5301 ATTGAGATAA TGTGGGAAAC TATATGAATC TTAAGGAAGT GGATCCTTTT  
5351 TTCTGTGGTC CTGCTCTCAC TCTCAAGTAT TAACTGATTG AATTTACTTC  
5401 TTCTGAAGGT GCGGTAGAGT TTAAGCTTTT TGTGTTGCC TTAACAAGC  
5451 AAGCCACTGA AAACGAGGTT GAGGAGGTAT GTCTCATATC CTACTTTTGT  
5501 ATGGAAAGTA ATTACTTATG TCTGATTTAC AAAGAGGGAA GCGTTCTAAA  
5551 TTTAGATATT ACAGTATCCC CTGTCGCCTT AGCTGGTAAT TTTAGTGATT  
5601 ATATGACAAAT TTAGTAGTCC TCTTGGAAGG GTCAGCGGCT TGAATTTTGT  
5651 TGTCAACTAT TCGAGCGCTT ACACATTTTA CTAAC TGAGT GATCTCTTCT

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Figure 8a Continued

5701 TTCAAATGGA CTGACTGAGT GATCTCTTCT TCCAAATGGA TGTAACTTTT  
5751 TGGCTGTCAG CTTTCTTTTC TCAGTAAATA TGATGAAGAT GTGAACGGCT  
5801 ACTTTGTCCT GTTGTGCTT TAACAGCTCT TTTTGCAATT TGGTCGCGTG  
5851 GAGGATGTCT ATCTCATGCG TGATGAATAT AGACAGAGTC GTGGTATGTC  
5901 TGGTAACTGC CACTAGACTC TATAACTCGT TTGATGGTGT TGATATGGTC  
5951 AAACGTGTTT TGACACTCAT TTAGGATGCG GGTTTGTTAA ATATTCAAGC  
6001 AAAGAGACGG CCATGGCAGC TATCGATGGT CTCAATGGAA CTTATACCAT  
6051 GAGAGTAAGC TGTGAAATCA CATGAGTATC TCACTTTCTC TGATTATCCC  
6101 CTCTAGACCT GTTTTGTTTA CTGGCCTCTT TCCCTTCTCC AGGGTTGCAA  
6151 TCAGCCATTG ATTGTTCCGT TTGCTGATCC AAAGAGGCCT AAACCGGGCG  
6201 AGTCAAGGTA TTGCCTTGGA GACTATATTT TGAATTCATT ATAATGCTAA  
6251 TATCAAAAAA ATTGTGTCTA CTGTCATTGT TTGTTCTATT GAGTTACATT  
6301 TATGAGAATC TTTTGGGGCA TGGGTGGAGG AGAGCTGCGA ACCTTATTC  
6351 TTCTCCAGTT ATTACTTGAA TGCGATGAAT TTCTTTCTAT ATATCCTTAA  
6401 CTAGTTTCTG TTTCCAGGGA AGTGGCACAT CCTGTTGGAC TTTGTTCAGG  
6451 GCCTCGTTTT CAAGCTTCAG GACCAAGGTG ACTGGGGTGA AAGGAGATCG  
6501 TTGTTTTTGT CATCAATTAA TTATATATTT TGAATAAACG TGGTCTCCTT  
6551 ATCTTCATTT GTTAGGCCTA CATCTAACCT TGGTGACCTT AGTGTGGATG  
6601 TGAGCCACAC AAATCCTTGG CGTCCTATGA ATTCACCAA CATGGGGCCA  
6651 CCTGGTAACA CTGGGATCCG TGGTACCGGA AGTGAATTGG CTCTAGGCC  
6701 AGGTCAAGCC ACATTACCTT CAAATCAGGT AAGAACAGCT TGATGATCAT  
6751 GTATATTATC TTATATGTAC ACACCCAATC ACACATAAAG TAATCGGGCA  
6801 TAAGGTTTTA CATGTATTGT GTGAGTAGGA CGAACATAAT TTATATGCTG  
6851 CACATATAAG AGCGTATGGA CTCTTGAAAA GAAGCATGAA GTTCCGACCT  
6901 TCCAGCTTTT CATATGATGC AGCAAACCTG ATGTGTTTTG CATTGAAATG  
6951 ATATGGCTTT GATTGTCATT TTGTCAGTTT CTAAGGAGTT TTTTCTTCA  
7001 ATAAATTTCTA CTCTGATGT TAGCTTTATT TGTGGCATTG TATAATGTAA  
7051 GGGAGGTCCA TTGGGTGGTT ATGTTGTTCC TGCCATTAAAC CCTCTACCAG  
7101 TCTCATCCTC TGCCACATCG CAACAGGTAC TTCAGCTGAA TTTTCCAAT

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Figure 8a Continued

7151 AAAGAAAATC TGAAAATGTT GTGTTGATCA GTTAATTTCA ACTGTTTCTA  
7201 TTCCATAGCA AAACCGGGGA GCTGGCCAGC ATATGTCACC ATTACAAAAA  
7251 CCTCTTCACA GTCCACAGGA TGTGCCCTT CGACCACAAA CTAATTTCCC  
7301 TGGGGCCCAA GCATCCTTGC AGAATCCTTA TGGTTATAGC AGCCAGTTGC  
7351 CTACTTCTCA GCTGCGGCCA CAACAAAACG TCACTCCTGC AACAGCTCCT  
7401 CAAGCTCCTT TGAACATCAA CCTACGGCCA ACACCTGTAT CTTCGTCAAC  
7451 TGATCAATTG CGCCCTCGTG CTCAGCAGCC ACCGCCACAA AAGATGCAAC  
7501 ATCCTCCTTC TGAGCTAGTT CAGCTCTTGT CACAACAGAC TCAGACTCTA  
7551 CAAGCAACCT TCCAATCATC TCAGCAAGCA TTTTCTCAAC TGCAGGAGCA  
7601 GGTGCAGTCC ATGCAGCAAC CAAACCAAAA ATTACCAGGC TCACAGACTG  
7651 GCCATGGTAA ACAGCAGGTA CAAACATAGT TCCCTGTTGC ATCTGTCCAG  
7701 TCCAGTTCCT CAGCTGTTTT TGTGTTTTTA ACTTACAATT ATTTCTGTAT  
7751 GTCTAAGTAT TCAATCCTTC ATATATTTTA GTAGTCCCTC TTTTTTATTA  
7801 TGTTTTTCTC GGTGCTTCT CTATCAGTGG GCTGGATCTG CAATTCCGAC  
7851 AGTTGTTAGC ACCACTGCTT CTACACCAGT TAGCTATATG CAAACAGCTG  
7901 CACCTGCAGC AACTCAGAGT GTTGTTTCTC GCAAATGTAA CTGGACCGAG  
7951 CATACCTCGC CTGATGGATT TAAGTATTAT TACAACGGTC AAACCGGTGA  
8001 AAGCAAGGTG AGAAACGTGG TTCCTCTTTA GTTATGTTCT CTTGTGAGTT  
8051 TCAGGAGGAT TCCTTGATATT TGCTGTGCTA TTTATTATCC TTGAACATGT  
8101 ATATGTATAG ATTTCAATATT TGAAGTTCAT CAATACGTGT CGTAATATAA  
8151 TTGACTTTTG CAGTGGGAAA AACCTGAGGA AATGGTATTG TTCGAACGTC  
8201 AGCAACAGCA GCCAACTATA AATCAGCCCC AGACCCAATC ACAGCAGGCT  
8251 CTTTATTCCC AGCCGATGCA GCAACAACCA CAACAGGTTC ACCAGCAATA  
8301 TCAGGGCCAA TATGTACAGC AGCCTATTTA TTCTTCAGTG GTTGGTCTCG  
8351 TTTTCTTGCT GCTTACATCC ATATAGTTTT CTCACATGGT CTCTAAGTTG  
8401 AATATGTATT CTMTCCATT TGGAGTTGCA GTATCCAACCT CCAGGGGTCA  
8451 GCCAGAATGC TCAGGTGTAT ATTTAGTTAA ATTATTGCT TATCTTTCAT  
8501 TTCAGAAATT GATCATTGAG TTACCAATCT AGTGGGTATA AGGAGACGGG  
8551 CCACTTTATG CAATAAACCA TGGTTTTACA AGCGTTTTGA ATATACAGAT

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Figure 8a Continued

8601 ACAAACATCT AAATTTGATC ATTTCAAAAT TTGATCATCG AGTTCCCTTT  
8651 TCAATGCAGT ATCCGCCGCC ATTGGGAGTT AGTCAAAATA GCCAGGTACA  
8701 TATTTGAACC TTATTTACAG TGGGACTAAT TGAAATTCGA TTTTGATATG  
8751 CATTTCATAA ATGTGAAGAT TTGATGAGTG GTCGTTTTGG TAGCGTTTTA  
8801 GAAAACGATA TGCATATATT CTCTAGTTGA ATATTTCTTT TTTCTGGAAC  
8851 ATGCAGTTTC CTATGTCAGG CACCGGTCAA AATGCTCAGG TACATATTAT  
8901 ATCATGCATC ATATCTTCTG ATTAAC TTCA AATTTAATCA GAAAACATAC  
8951 GTGAGATTCC AGTAGAAACA AAATCGATAT GACTGTATTG GTTGGAAATG  
9001 GTTAAGGCAG AGCTCATGTT CTAATGTGTT AAAATTTTCT AGGAATTT

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Figure 8b

1 MGYGFDGGFP PMSRDGGFWP NVPVNFPPSE SPDAGGYSGG RGFQSTGPAY  
51 SVRLTSPPIQ QPLSGQKRGR PLSEQSSFTG TGLLIVAVMV KLFVGSVPRT  
101 ATEEEVRPFS NNTVNVLEVA FIKDKRTGQQ QGCCFVKYAT SEDADRAIRA  
151 LHNQITLPGG TGLVQVRYAD GERERIGAVE FKLFGVSLNK QATENEVEEL  
201 FLQFGRVEDV YLMRDEYRQS RCGGFVKYSS KETAMAAIDG LNGTYTMRGC  
251 NQPLIVRFAD PKRPPKPGESK EVAHPVGLCS GPRFQASGPK PTSNLGDLSV  
301 DVSHTNPWRP MNSPNMGPPG NTGIRGTGSD LAPRPGQATL PSNQGGPLGG  
351 YVVPAINPLP VSSSATSQQQ NRGAGQHMSF LQKPLHSPQD VPLRPQTNFP  
401 GAQASLQNPY GYSSQLPTSQ LRPQQNVTPA TAPQAPLNIN LRPTPVSSAT  
451 DQLRPRAQQP PPQKMQHPPS ELVQLLSQQT QTLQATFQSS QQAFSQLQEQ  
501 VQSMQQPNQK LFGSQTGHGK QQWAGSAIPT VVSTTASTPV SYMQTAAPAA  
551 TQSVVSRKCN WTEHTSPDGF KYYYNGQTGE SKWEKPEEMV LFERQQQQPT  
601 INQPQTQSQQ ALYSQPMQQQ PQQVHQYQYQ QYVQQPIYSS VYPTPGVSQN  
651 AQYPPPLGVS QNSQFPMSGT GQNAQ

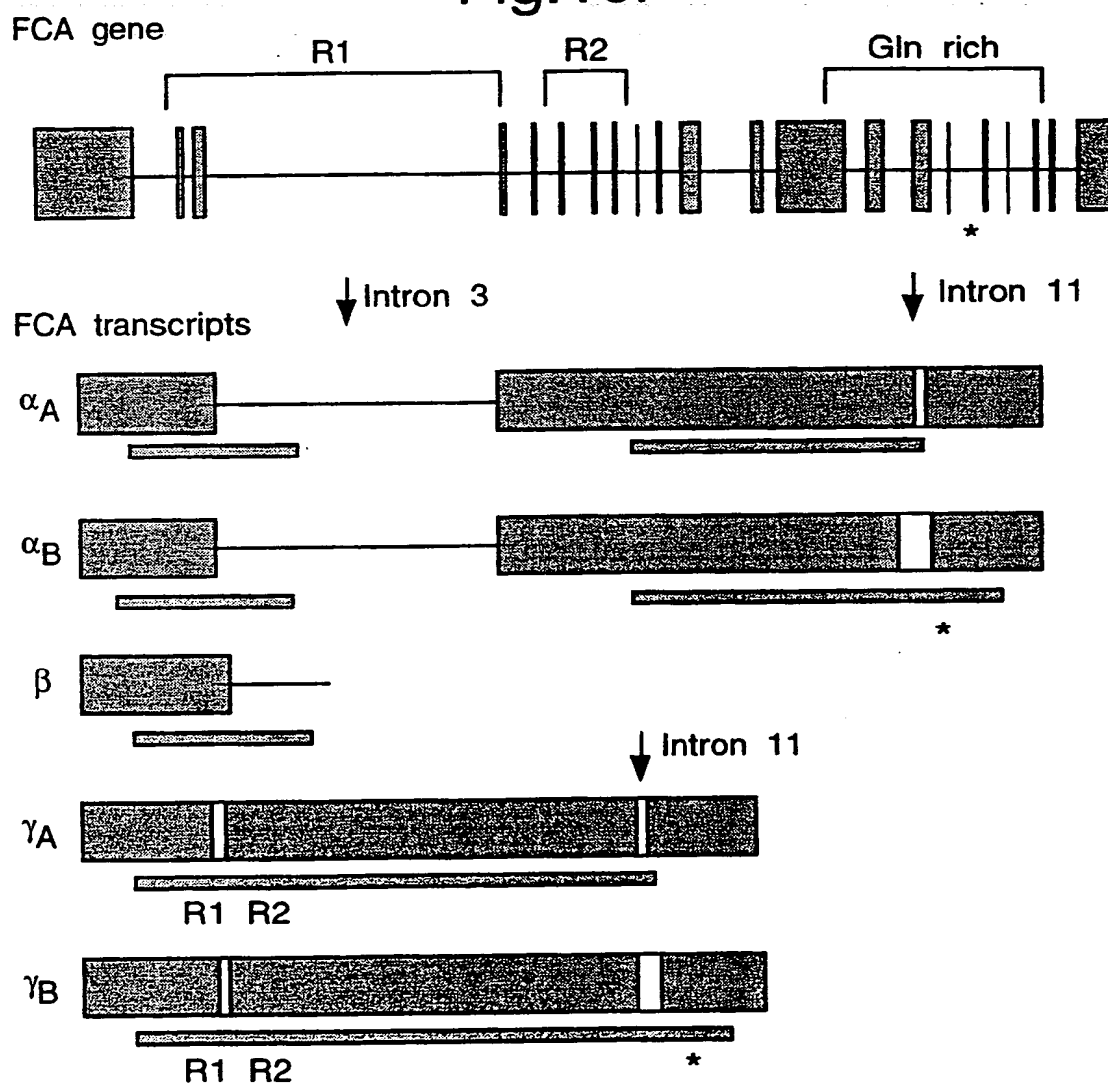
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Fig.10.



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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/29, 15/82, C07K 14/415,</b> <b>A01H 5/00</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 96/38560</b> <b>(43) International Publication Date:</b> 5 December 1996 (05.12.96)
<b>(21) International Application Number:</b> PCT/GB96/01332 <b>(22) International Filing Date:</b> 3 June 1996 (03.06.96)  <b>(30) Priority Data:</b> 9511196.9                      2 June 1995 (02.06.95)                      GB  <b>(71) Applicant (for all designated States except US):</b> JOHN INNES CENTRE INNOVATIONS LIMITED [GB/GB]; Norwich Research Park, Colney Lane, Norwich NR4 7UH (GB).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> DEAN, Caroline [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). MACKNIGHT, Richard, Colin [NZ/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). BANCROFT, Ian [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB). LISTER, Clare, Katharine [GB/GB]; John Innes Centre, Molecular Genetics Dept., Norwich Research Park, Colney, Norwich NR4 7UH (GB).  <b>(74) Agents:</b> WALTON, Seán, M. et al.; Mewburn Ellis, York House, 23 Kingsway, London WC2B 6HP (GB).	<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the</i> <i>claims and to be republished in the event of the receipt of</i> <i>amendments.</i>  <b>(88) Date of publication of the international search report:</b> 9 January 1997 (09.01.97)	
<b>(54) Title:</b> GENETIC CONTROL OF FLOWERING  <b>(57) Abstract</b>  <p><i>FCA genes of Arabidopsis thaliana and Brassica napus are provided, enabling flowering characteristics, particularly timing of flowering, to be influenced in transgenic plants. Timing of flowering may be delayed or hastened using sense and antisense expression, also various mutants and alleles, including alternatively spliced forms.</i></p>		

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## INTERNATIONAL SEARCH REPORT

International Application No

PC1/GB 96/01332

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/29 C12N15/82 C07K14/415 A01H5/00

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## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ANNUAL MEETING OF THE SOCIETY FOR EXPERIMENTAL BIOLOGY, BIRMINGHAM, ALABAMA, USA, APRIL 7-12, 1991. J EXP BOT 42 (238 SUPPL.). 1991. 48., XP002018457 BANCROFT I ET AL: "THE DEVELOPMENT OF SYSTEMS FOR THE ISOLATION OF GENES FROM ARABIDOPSIS-THALIANA BY CHROMOSOME WALKING IN YAC LIBRARIES TOWARDS THE ISOLATION OF THE FLORAL INDUCTION GENE FCA." see abstract P8.62 --- -/--	1-14,28, 29, 31-37,39

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Date of the actual completion of the international search

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
O,X	JOURNAL OF EXPERIMENTAL BOTANY, vol. 45, no. 278, September 1994, pages 1279-1288, XP000609516 CHANDLER, J., ET AL.: "Factors influencing the vernalization response and flowering time of late flowering mutants of Arabidopsis thaliana (L.) Heynh." see page 1288, right-hand column & THIRD INTERNATIONAL CONGRESS OF PLANT MOLECULAR BIOLOGY: MOLECULAR BIOLOGY OF PLANT GROWTH AND DEVELOPMENT. TUCSON, ARIZONA. ABSTRACT NO. 508, 1991, WESTPHAL, L., ET AL.: "Cloning FCA, a late-flowering locus of Arabidopsis thaliana (L.) Heynh." ---	1-14,28, 29, 31-37,39
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P,X	SEMIN. CELL DEV. BIOL. (1996), 7(3), 435-440 , XP000609514 WILSON, ALLISON ET AL: "Analysis of the molecular basis of vernalization in Arabidopsis thaliana" see page 436, right-hand column - page 437, left-hand column ---	1-4, 8-10,29, 30
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A	MOLECULAR AND GENERAL GENETICS, vol. 229, 1991, pages 57-66, XP002018289 KOORNNEEF, M., ET AL.: "A genetic and physiological analysis of late flowering mutants in Arabidopsis thaliana" cited in the application see the whole document --- -/--	1-40

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## INTERNATIONAL SEARCH REPORT

International Application No

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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